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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Dec 18 18:14:18 1998; MasPar time 50.54 Seconds 935.076 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score Sequence: >US-08-951-733-14 (1-949) from US08951733.pep (1 of 2) 7113

Score: HASGQRCVLLRTWEALAPAT.....PVEDEALGGTAFVQMPAHGL 949

Scoring table: PAM 150 Gap 11

Searched: 165420 segs, 49795644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb16
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_incertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 53.273; Variance 101.693; scale 0.524

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

110 110 110 110 110 110 110 110 110 110	Result
6954 6987 4087 675 675 432 432 432 147 147 147 141 143 136 136 137 135 135 135	Score
97.8 97.5 9.5.5 9.5.5 9.5.5 9.5.5 9.5.5 9.5.5 1.9.9 1.9.9 1.9.9 1.9.9	% Query Match
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111 3 3 114 114 114 114 114 114	DB
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ALIGNMENTS

Db 241 GAAPEPERTPVGQGSWAHPGRTRGPS	Db 181 ATQARPPPHASGPRRIGCERAWNHS	Db 121 SYLPNTVTDALRGSGAWGLLLRRVGI 	Db 61 DARPPPAAPSERQVSCLKELVARVLG	Db 1 MPRAPRCRAVRSLLRSHYREVLPLAY	Query Match 97.8%; Sco Best Local Similarity 100.0%; Pro Matches 927; Conservative 0;	RNA-DIRECTED DNA POLYMERA SEQUENCE 1132 AA; 1269	LINGNER J., HARLEY C SCIENCE 277:955-959(EMBL: AF015950: G233	RC TISSUE-KIDNEY; RX MEDLINE; 97400623. RA NAKANURA T.M., MORIN G.B., CHAPMAN K.B.,	RP SEQUENCE FROM N.A.	EUKARYOTA; METAZOA; CHORDATA; EUTHERIA; PRIMATES.	OS HOMO SAPIENS (HUMAN).	TELOMERASE REVERSE TRANSCRI	DT 01-JAN-1998 (TREMBLREL, 05, LAST O1-JUN-1998 (TREMBLREL, 06, LAST	01-JAN-1998 (TREMBLREL. 05,	O14745 TRELIMINARY;	O14746 PRELIMINARY;
GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300	ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240 	SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180 	DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120 	MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGÞQGWRLVQRGDÞAAFRALVAQCLVCVÞW 60 	Score 6954; DB 4; Length 1132; Pred. No. 0.00e+00; 0; Mismatches 0; Indels 0; Gaps 0;	4; 2DFBEDF3 CRC32;		APMAN K.B., WEINRICH S.L., ANDREWS W.H.,		VERTEBRATA; TETRAPODA; MAMMALIA;			AST SEQUENCE UPDATE)	(ED)		PRT; 1132 AA.

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MEDLINE, 97433088.

MEYERSON M., COUNTER C.M., EATON E.N., ELL.
CADDLE S.D., ZIAUGRA L., BEIJERSBERGEN R.L.
BACCHETTI S., HABER D.A., WEINBERG R.A.;
CELL 90:785-795(1997).

EMBL; AF018167; G2347129; -.
SEQUENCE 1132 AA; 126937 MW; C1E5E2AF
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larity 99.9%;
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Best Loc
Matches
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GREENBERG R.A., ALLSOPP R.C.,
ONCOGENE 0:0-0(1998).
EMBL; AF051911; G3005592; -.
RNA-DIRECTED DNA POLYMERASE.
SEQUENCE 1122 AA; 127977 M
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 849
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                                                                                                                                                                                                         LQPNLTGARRLVEIIFLGSRPRTSGPLCRTHRLSRRYWQMRPLFQQLLVNHAECQYVRLL
                                                                                                                                                                                                                                  DLSLS-GSVCCKHKPSSTSLLSPPRQNAFQLRP-FIETRHFLYSRGDGQERLNPSFLLSN
                                                                                                                                                                                                                                                                                   TTDIWPSVSASYRPTRPVGRNFTNLRFLQQIKSSSRQEAPKPLALPSRGTKRHLSLTSTS
 QCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRT
                                                                                                                                                                                                  LRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLL
                                                                                                                                                                                                                            GTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGD-KEQLRPSFLLSS
                                                                                                                                                                                                                                                                            ATQARPPPHAS-GPRRRLGCE-RA-W--NH---SVR-EAGVPLGLPAPGARRRGGSASRS
                                                                                                                                                                                                                                                                                                                                                                           h 57.5%;
Similarity 61.0%;
574; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 RODENTIA
                                                                                                                                                                                                                                                                                                                                                                                                                             ALLSOPP R.C.,
                                                                                                                                                                                                                                                                                                                                                                            Score 4087; DB 11;
Pred. No. 0.00e+00;
169; Mismatches 163;
                                                                                                                                                                                                                                                                                                                                                                                                      MW;
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Best Local S
Matches 12
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013339;
01-JAN-1998
01-JAN-1998
01-AUG-1998
TELOMERASE RI
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013338;
01-JAN-1998
01-JAN-1998
01-JUN-1998
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EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
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Local Similarity 26.7%;
les 125; Conservative
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||:||||||:||:||:|||||
LVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGL
                                                                                                                                           FITVNKKDAKKFLNLSLRGFEKHNFSTSLEKTVINFENSNGIINNTFF
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                                                                                                                                                                     MCHHAVRIRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDG-LLLRLVDDFL
                                                                                                                                                                                         LSGHIVKIGNSQYLQKVGIPQGSILSSFLCHFYMEDLIDEYLSFTKKKGSVLLRVVDDFL 746
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                   8 (TREMBLREL. 05, CREATE
8 (TREMBLREL. 05, LAST S
8 (TREMBLREL. 07, LAST A
REVERSE TRANSCRIPTASE 1
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8 (TREMBLREL. 05, LAST 08 (TREMBLREL. 06, LAST 08)
REVERSE TRANSCRIPTASE
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                     REVERSE
                                                                             PRELIMINARY;
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Pred. No. 2
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                              SEQUENCE UPDATE)
ANNOTATION UPDAT
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Mismatches 196;
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2.26e-10
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                                  UPDATE)
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SCHIZOSACCHAROMYCES POMBE

(FISSION YEAST).

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Best Local S
Matches 12
                                                                                         01-JUL-1997 (TREMBLREL. 04, CREATED)
01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCOL-1, 1998 (TREMBLREL. 05, LAST ANNOTAL
TELOMERASE SUBUNIT P123.
EUPLOTES AEDICULATUS.
EUKARYOTAE; MITOCHONDRIAL EUKARYOTES; A.
HYPOTRICHS; EUPLOTIDA; EUPLOTES.
                        SEQUENCE FROM N.A.
MEDLINE; 97274210.
LINGNER J., HUGHES T
CECH T.R.;
                                                                                                                                                                                                         O00939
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EMBL; AF015783; G2340168; -.
EMBL; AL022299; E1285360; -.
PFAM; PF00078; rvt.
RNA-DIRECTED DNA POLYMERASE.
 EMBL;
           CECH T.R.;
SCIENCE 276:561-567(1997).
                                                                                                                                                                                               000939;
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NAKAMURA T.M., MORIN G.B., CHALINGNER J., HARLEY C.B., CECH SCIENCE 277:955-959(1997).
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   717
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                                                                                                                                                                                                                                                                                                                    HHAVRIRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDG-LLLRLVDDFLLV 895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EWLVLGKRSNAKMCLSDFEKR-KQ-IFAEFIYWLYNSFIIPILQSFFYITESSDLRNRTV 457
                                                                                                                                                                                                                                                                 TPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAF
                                                                                                                                                                                                                                                                                   TVNKKDAKKFLNLSLRGFEKHNFSTSLEKTVINFENSNGIINNTFF 793
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NMDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFV
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                                                                                                                                                                                                                                                                                                                                               GHIVKIGNSQYLQKVGIPQGSILSSFLCHFYMEDLIDEYLSFTKKKGSVLLRVVDDFLFI 747
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U95964; G2072336;
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                                                                                                                                                                                                            PRELIMINARY;
                                         T.R.,
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                                           SHEVCHENKO
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                                           Α:
                                                                                                             ALVEOLATA; CILIOPHORA;
                                           MANN
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                                         LUNDBLAD
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T 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPLA.
DT 01-JAN-1998 (TREMBLEEL. 07, LAST ANNOTATION UP
DT 01-AUG-1998 (TREMBLEEL. 07, LAST ANNOTATION UP
DE TELOMERASE CATALYTIC SUBUNIT (FRAGMENT).
OS MUS MUSCULUS (MOUSE).
OS EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TET
CHURCHERIA; RODENTIA.
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Best Local S
Matches 5
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Best Local
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                                                                                                                                                                                                                                     DRISSI R., CLEVELAND J.L.;
SUBMITTED (OCT-1997) TO EMBL/GENBANK/DDBJ
EMBL; AF029235; G2605903; -.
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                                                 642
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                                                                                                              FFYVTESTFQKNRLFFYRKSVWSKLQSIGVRQHLERVRLRELSQEEVRHHQDTWLAMPIC
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                                                 RLRFIPK
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                                                                                                 FFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QDPPPELYFYKYDYTGAYDTIPQDRLTEYI-AS-IIKPQ---NTYCV--RRYAVY-Q-KA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QVGQPKLFFATMDIEKCYDSVNREKLSTFLKTTKLLSSDFWIMTAQILKRKNNIVIDSKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RTFRREKRAERLTSRVKALFS--VLNYERARR-PGLLGASVLGLDDIHRAWRTEVLRVRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KIVNSDRKTTKLTTNTKLLNSHLMLKTLKNRMFKDPFGFAVFNYDDVMKKYEEFVCK-WK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWS
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                                                                                                                                                Similarity
51; Conse
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                                                                                                                                                                                                67 AA;
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llarity 25.2%;
Conservative
                                                                                                                                                6.0%;
llarity 76.1%;
Conservative
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8368 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 432; DB 5;
Pred. No. 2.78e-58;
122; Mismatches 194
                                                                                                                                                                                                                                                                                                                                      CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
T (FRAGMENT).
                                                                                                                                                Score 424; DB 11;
Pred. No. 1.11e-56;
10; Mismatches 6;
                                                                                                                                                                                                  E2A06F2B CRC32;
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                                                                                                                                                                                                                                                                                                              TETRAPODA; MAMMALIA;
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                                                                                                                                                                                                                                                   BANKS
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01-NOV-1996 (TREMBLREL 01, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL 07, LAST ANNOTATION UPDATE)
CHROMOSOME XII COSMID 8543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA EMBL; U20618; G662136; -. SEQUENCE 884 AA; 102662 MW; 1A94320F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHERRY J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-S288C (AB972);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=S288C (AB972);
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WEDLER H., ZIMMERM.
NATURE 387:0-0(0).
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MEDLINE; 97313267.
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EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
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     822
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                                                                                                                                                                                                                                                                QIADRI-KEFKQRLLKKFNNVLPELYFMKFDVKSCYDSIPRMECMR-ILKDALKNENGFF
                                                                                                                                                                                                                                                                                                                                                                          | :| | | : | | : | :| :| : | : :::| : ::| : ::| :: | ::: | :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| :::| ::
     EASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTLLCSLCYGDM-E-NKLF-
                                   E---M-EIF-K-T---ALWVEDKCYIREDGLFQGSSLSAPIVDLVYDDLLEFYSEFKAS
                                                                                                             VR-RYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLN
                                                                                                                                                                     VRSQY-FFNTNT-G-VLKLFNV-VNASRVPKPY-ELYIDNVR-TVHLSNQDVIN---VV-
                                                                                                                                                                                                                             DI-HRAWRTFVLRV-RA-QDPPPELYFVKVDVTGAYDTIPQ-DRLTEVIASIIKPQNTYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STVTIVYF-RHDTWNKLITPFIVEYFKTY-LVE-NNV-CRNHNSYTLSNFNHSKMRIIPK 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 4.4%;
1 Similarity 24.3%;
118; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 314; DB 3; Le
Pred. No. 3.84e-35;
122; Mismatches 202;
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AC OC
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D Q69118;
C Q69118;
C Q69118;
O1 - NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01 - NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01 - NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL PROTEIN (FRACMENT).
OS HUMAN HERESVIEUS TYPE 4.
OS VIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE;
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Best Local S
Matches 4
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Best Local
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000600
000600;
01-JUL-1997
01-JUL-1997
01-JUL-1997
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MEDLINE; 87284169.

PFITZNER A.J., TSAI E.C., STROMINGER J.L.,
J. VIROL. 61:2902-2909(1987).

EMBL; M17294; G807646; -.

EMBL; M17294; G807611N.
                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                               AZEN E.A., AMBERGER E., FISHER S., AM. J. HUM. GENET. 58:143-153(1996) EMBL; S80916; G1911492; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE; 96108975.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUTHERIA; PRIMATES
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HPGKPEGPPPQEGNKSKSARSPPGKPQGPPQQEGNKPQGPPPPGKPQGPPPPGGNPQQPQ
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                                                                                                 QLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPK
                                                                                                                                         QGGNQSQG-PPPHPGKPERPPP-QGG-NQSHRPPPPPP-GKPER-PPPQGGNQSQG-P-PP
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Similarity 28.2%;
40; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                     234 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        296 AA;
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llarity 38.6%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                        23656 MW;
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04, LAST SEQUENCE UPDATE)
04, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                           Score 142; DB 4; Le Pred. No. 3.60e-05; 41; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 147; DB 14; 1
Pred. No. 6.53e-06;
20; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                        B5920075 CRC32;
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Best Local (
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THESIS (1995), UNIVERSITAET B.
EMBL; X78052; G459248; -.
EMBL; X81893; E258949; -.
SEQUENCE 276 AA; 31718 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              054226;
054226;
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Q46612;
Q1-NOV-1996
                                 SALAH-BEY K., DOUMITH M., MICHEL J.M., HAYDOCK S., CC
LEADLAY P.F., RAYNAL M.C.;
SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; Y14332; E1228185; -.
                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1998 (TREMBLREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
POLYKETIDE SYNTHASE (FRAGMENT).
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01-NOV-1996 (TREMBLEEL. 01, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
IS 1222 GENE ORF-A AND ORF-B.
                                                                                                                                                                                                                                                                                                                        SACCHAROPOLYSPORA ERYTHRAEA (STREPTOMYCES PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-KLEEBERGER, 1983;
MEDLINE; 95255664.
                                                                                                                                                                                                                    STRAIN-NRRL2338;
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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GENE 156:37-42(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENTEROBACTER AGGLOMERANS
       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLL-RPAAPNLTWSDDFVMDALATGRRIK 126
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30; Conser
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       373
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larity 33.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIDDAVATTAM D.;
   ₽,
   40872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31718 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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   Œ;
                                                                                                                                                                               MICHEL J.M., HAYDOCK S., CORTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCOTOBACTERIA; FACULTATIVELY ANAEROBIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 141; DB 2; Lei
Pred. No. 5.04e-05;
23; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BAYREUTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLINGMUELLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0B54A420 CRC32;
   781BEC6D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         276
                                                                                                                                                                                                                                                                                                                            NOCARDIOFORM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>ن</u>
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RESULT 14
ID Q99076
AC Q99076;
AC Q99076;
DT 01-NOV-1996 (TREMBLREL 01, C)
DT 01-VOV-1996 (TREMBLREL 01, L)
DT 01-UUN-1998 (TREMBLREL 06, L)
DT 01-UUN-1998 (TREMBLREL)
DE HOMEOBOX PROTEIN (FRAGMENT).
GN HB9.
OS HOMO SAPIENS (HUMAN).
CC EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
ID 036027;
AC 036027;
A
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Best Local S
Matches 4
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O36027;
O1-JUN-1998 (TREMBLREL. 06
O1-JUN-1998 (TREMBLREL. 06
O1-JUN-1998 (TREMBLREL. 06
MISKOTT-ALDRICH SYNDROME P
WSF1 OR SPAC4F10.15C.
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DOMAIN
DOMAIN
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONNOR R., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-I- SIMILARITY: TO YEAST LAS17.
EMBL, AF038575, G2708709; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-JS21;
ZANKEL T.C., OW D.W.;
SUBMITTED (DEC-1997)
HOMO SAPIENS (HUMAN).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               305 AANKKRPPPPPPP-PSRR---NRG-KPPIGNGSSNSSLPPPPPPPRSNAAG-SIPLPPQGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         335 PPRP 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 PRRRAA-NRRRG-AAPAPGIAPG-AAHG-HRRG-AARRARDRRRRGGRGRRRGGQPRPGG
                                                                                                                                                                                                                                                                                                                    321
                                                                                                                                                                                                                                                                                                                                                                  417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298 L-RRARPPR-RGPPRRRPRAYGTSRPPRQAGG-AGH-R-ARHRRTA-GRGQGAARTHAQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               y Match 2.0%;
Local Similarity 32.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGRP
                                                                                                                                                                                                                                                                                                                    VGRQHHAGPPSTSRPPRPWDTPCPPV
                                                                                                                                                                                                                                                                                                                                                                VPTPP-SLPPSAPPSLPPSAPPSLPM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAPPPPPPRSAPSTGROPPPLSSSRAVSNPP--APPPAIPGRSAPALPPLGNASRTSTPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATQARPPPHASGPRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Z98980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      574 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                311
337
361
248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.0%;
larity 28.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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06, LAST SEQUENCE UPDATE)
06, LAST ANNOTATION UPDAT
E PROTEIN HOMOLOG 1.
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                                                                                                           CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 143; DB 3; Pred. No. 2.56e-05; 41; Mismatches 53
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Pred. No. 7.05e-05;
27; Mismatches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY-PRO.
L -> V (IN STRAIN JS21).
; 9E84D37C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLY-PRO.
POLY-PRO.
                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                  441
                                                                                                                                                                                                                316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WOOD V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       320
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                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.9%;
Best Local Similarity 26.4%;
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 1.9%;
Best Local Similarity 30.9%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

STRAIN=CD-1; TISSUE-LIVER;

MEDLINE: 88273214.

ANN D.K., SMITH M.K., CARLSON D.M.;

J. BIOL. CHEM. 263:10887-10893(1988).

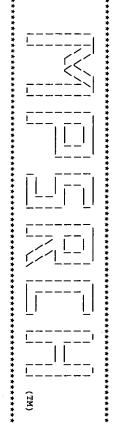
EMBL; M23236; G567232; -.

MCD; MGI:97773; PRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA_BIND
DNA_BIND
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFAM; PF00046; homeobox.
DNA-BINDING; NUCLEAR PROTEIN; HOMEOBOX; PHOSPHORYLATION.
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                                                                                                       318
                                                                                                                                            154 GGPQPRPPQGPPPPAGPQPRPPQGPPPP 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          223 RAWNHSVREAGV-PLGLPAPGARRRGGSASRSLPLPKRPRRG-AAPEPERTPVGQGSWAH 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202 RPWSTASSDCSVGRTGIAPRGPAT-SPRPSRSPAAQDRSRPARSAPGPAASPGGPGAWTH 260
                                                                                                                                                                                                               259
                                                                                                                                                                                                                                                            95 PPPGGPQPRPPQGPPPPGG-PQPRPPQGPPPPGGPQGPPPPGGPQQRPPQGPPPP 153
                                                                                                                                                                                                                                                                                                                                           HPSVGRQHHAGPPSTSRPPRPWDTPCPP 345
                                                                                                                                                                                                            RPRRGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPAR-PAEEATSLEGALSGTRHS 317
                                                                                                                                                                                                                                                                                                              AATQARPPPHAS--GPRRRLGCE-RAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPK 258
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316 AA;
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16 317 I
317 AA; 31719 MW;
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121
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                                                                                                                                                                                                                                                                                                                                                                                                              Score 132; DB 11; Length 317; pred. No. 9.90e-04; 38; Mismatches 64; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 136; DB 4; Length 316; Pred. No. 2.67e-04; 20; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HOMEOBOX.
H-T-H MOTIF.
1531E766 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.

PROLINE-RICH PROTEIN.

10C84341 CRC32;
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Run MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Fri Dec 18 18:34:59 1998; MasPar time 9.57 Seconds 508.951 Million cell updates/sec

Tabular output not generated

Description: Perfect Score: (640-940) from US08951733.pep (2 of 2) 2214 >US-08-951-733-14

TSRLRFIPKPDGLRPIVNMD......NLRKTVVNFPVEDEALGGTA 301

Scoring table: Gap 11 PAM 150

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Listing Match 0% first 45 summaries

Database:

a-geneseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29

Statistics: Mean 34.011; Variance 149.700; scale 0.227

Pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed. and is derived by analysis of the total score distribution.

SUMMARIES

1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
109 97 97 97 90 90 90 90 90 90 90 90 90 90 90 90 90	Score
44444446000000000000000000000000000000	Query Match I
370 903 1398 1398 785 785 420 423 423 421 421 1784 1784 1784 1784 1784 1784 1784 1784 1784 1784 1784 1788 1785 1702 170	Length
116 116 117 116 116 117 116	BB
W20923 W241007 W24124 R87008 W16303 W15927 W25926 W25926 W25927 W25927 W23652 W25927 W24792 W25927 W2592	ID
H. pylori cytoplasmic Hyperthermostable pro Pyrococcus furiosus protease. Yeast mitochondria CO Xenopus melatonin rec Xenopus melatonin solitari red product of first M.tuberculosis small r. litoralis subtilis srf gClq receptor. Prod. of gene partici	Description
2.55e+00 1.85e+01 1.85e+01 1.85e+01 1.85e+01 5.64e+01 5.64e+01 5.64e+01 5.64e+01 5.64e+01 7.72e+02 9.01e+01 7.72e+02 9.01e+	Pred. No.

Query Match 4.9%; Best Local Similarity 25.0%; Matches 17; Conservative

Score 109; DB 22; 1 Pred. No. 2.55e+00; 23; Mismatches 24;

Length 370; Indels

4

Gaps

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45	44	43	42	41	40	39	38	37	36	3 5	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	L
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W41262	R97245	R70148	W14920	W18792	R10051	W28502	W28503	W24230	R60782	R60786	R60784	W24228	R60788	W23138	W24229	P90419	R87723	W06421	W06422	R63633	R63631	R60252	R30729	R25591	R78183	K/GTGT
Apolipoprotein B-100.	Virulence gene cluste		Berolina potato starc	Starch binding protei	ltodext		grass	ū	$\overline{}$		HIV virus-1(LAI) gp12	Human melanoma associ	HIV virus-1(LAI) gp12	Protease inhibitor.	Human melanoma associ	Plasmodium falciparum	Full length coconut L		ſΛ	Murine receptor-type		NF-ATP.	rotein from	RING11 antigenic pept	Human RAD51 protein,	Mouse Kappi procein,
1.93e+02				2.25e+02	:	:		1.66e+02			1.93e+02			_	1.66e+02	-	:.	1.93e+02	1.93e+02	1.43e+02	1.43e+02	1.23e+02	1.43e+02	1.23e+02	1.23e+02	1.23e+02

ALIGNMENTS

The present sequence is a H. pylori cytoplasmic protein.

CC The present sequence is a H. pylori cytoplasmic protein.

CC infection or to identify H. pylori polypeptide binding compounds,

CC useful as potential H. pylori life cycle activators or inhibitors.

CC verlaping contigs generated by mechanically shearing the bacterial

CC overlapping contigs generated by mechanically shearing the bacterial

CC overlapping contigs generated by mechanically shearing the bacterial

CC and the predicted coding regions defined by computer evaluation. To

CC and the predicted coding regions defined by computer evaluation. To

CC identify likely H. pylori antigens for vaccine development, the amino

CC acid sequences predicted from various ORF were analysed for significant

CC homology to other known or exported membrane proteins. Having identified

CC and determined the sequences of interest, particular regions can be

CC isolated from H. pylori by PCR amplification for recombinant polypeptide

CC Sequence 370 AA; H. pylori cytoplasmic protein, 16ae10508orf10. Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; envelope. Helicobacter pylori. w09640893-A1. Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter Claim 61; Page 1321-1322; 1481pp; English. W20923 standard; protein; W20923; N-PSDB; T68716 Berglindh OT, 01-APR-1996; 06-JUN-1996; 07-JUN-1995; (ASTR) ASTRA AB. 21-JUL-1997 (first entry) 97-052306/05. US-630405 U09122 US-487032. Smith D, Mellgaerd BL; 370 AA.

Matches

17;

Conservative

15;

Mismatches

22;

Indels

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Gaps

4

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Matches 1
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                                                                                                                                           used as i
                                                                                                                                                              Protease(s) and genes encoding them obtained from Thermococcus and Pyrococcus strains - have extremely high thermal stability and are useful industrially and as research reagents Disclosure; Page 100-108; 159pp; Japanese.

This sequence represents the protease from Pyrococcus furiosus. This sequence is a protease of the invention. The proteases of the invention have extremely high thermal stability. The proteases can used as research reagents, and industrially in the food, drug and
                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; T95670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tsunasawa S, Yamamo
WPI; 97-332794/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Asada K, Kato I, Mitta M, Morishita M, Takakura
Tsunasawa S, Yamamoto K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-JUN-1997.
07-NOY-1996; J03253.
12-DEC-1995; JP-323285.
(TAKI ) TAKARA SHUZO CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pyrococcus furiosus WO9721823-A1.
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Claim 2; Page 43-48; 85pp; Japanese.
A hyperthermostable protease (R87007) is encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pyrococcus furiosus hyper:thermostable purecombinant prodn. of hyper:thermostable
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N-PSDB; T08141.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-DEC-1995.
05-JUN-1995; J01095.
13-JUN-1994; JP-130236.
26-JUL-1994; JP-173912.
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                                                                                                     as research reagents, itcal industries. ence 1398 AA;
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29
Score
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Pred.
15; M
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97;
No.
   DB 27;
1.85e+01;
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1.85e+01
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Similarity

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Best Local
the cleaved strand
Disclosure; Page 40-42; 58pp; English.

Yeast mitochondrial COXI gene intron aIZ-encoded protein (W16303)
can be used in a novel method for cleaving a double-stranded or
single-stranded DNA substrate. The method utilises a nucleotide
integrase, pref. a (reconstituted) ribonucleoprotein (RNP) particle
comprising an excised RNA transcript encoded by the group II intron
aIZ (see also T63319) of the COXI gene and a protein encoded by the
group II intron aIZ of the COXI gene. The RNP is incubated with the
DNA substrate in the presence of a divalent cation so that at least
one strand of the DNA substrate is cleaved and a nucleic acid
The course is attached to one or both of the cleaved strands. The
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(OHIO-) OHIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pyrococcus furiosus hyper:thermostable protease gene - useful recombinant prodn. of hyper:thermostable protease Example 2; Page 57-64; 85pp; Japanese. The invention relates to a gene (T0814) that codes for a hyperthermostable protease (R87007) of Pyrococcus furiosus. A related DNA sequence (T08132) includes the coding sequence of the protease gene and encodes a protein (R87008) that
                                                                                                                                                                                                                                                                                                                                                                                Guo H, Lambowitz AM, WPI; 97-202256/18. N-PSDB; T63319.
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R87008;
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WPI; 96-049674/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TAKI ) TAKARA SHUZO CO LTD.
Asada K, Kato I, Mitta M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-JUN-1994;
26-JUL-1994;
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llarity 29.38;
Conservative
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STATE RES
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JP-173912.
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15; M
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06-FEB-1997.
24-JUL-1996; E
24-JUL-1995; E
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also be u
Sequence
        New nucleic acid encoding functional melatonin receptor of Xenopus for screening for potential (ant)agonists useful for e.g. treating cardiovascular disease and cancer Claim 5; Page 25-26; 62pp; French.
Sequences W25926-7 represent novel allelic Xenopus laevis melatonin receptor MEL-1A proteins. This sequence is a new form of the melatonin receptor designated MEL-1AA, hals sequence as Mel 1-c(alpha). The protein differs from previously known receptors by being 65 amino acids shorter and also having 2 different C-terminal amino acids. The protein is encoded by 2 different alleles (T79063-4) which differ in the 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus melatonin receptor MEL-1Aa.

Allele; Xenopus laevis; melatonin; receptor; untranslated region; PCR; mRNA; half-life; skin; amplification; primer; polymerase chain reaction; transmembrane domain; cellular signalling; inhibition; adenylyl cyclase;
                                                                                                                      (ADIR ) ADIR & CIE. Jockers R, Marullo S, WPI; 97-132635/12.
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larity 44.4%;
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33..56
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e= "transmembrane
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Pred.
7; M
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24-JUL-1996; F01167.
24-JUL-1995; FR-008947.
(ADIR ) ADIR & CIE.
Jockers R, Marullo S,
WPI; 97-132635/12.
New nucleic acid encoding functional melatonin receptor of Xenopus for screening for potential (ant)agonists useful for e.g. treating cardiovascular disease and cancer Claim 5, Page 30-31; 62pg; French.
Sequences W25926-7 represent novel allelic Xenopus laevis melatonin receptor MEL-la proteins. This sequence is a new form of the melator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenopus melatonin receptor MEL-1Ab. Allele; Xenopus laevis; melatonin; mRNA; half-life; skin; amplificatio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA; half-life; skin; amplification; primer; polymerase chain react
transmembrane domain; cellular signalling; inhibition; adenylyl cyci
modulation; intracellular; cyclic GMP; inhibitor; phosphodiesterase
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Sequence 354 AA;
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W23652;
09-OCT-1997
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T 9
8409 standard; Protein; 420
R88409;
15-AUG-1996 (first entry)
                                                                                                                                                                                                                                                                                                       The present sequence represents a recombinant squirrel protease inhibitor protein 55RS that contains a specifically claimed reaction site, see features table. The protease inhibitor 55RS has inhibitory activity against trypsin, elastase or thrombin. The protease inhibitor has a new structure similar to alpha-1-antitrypsin and shows selective inhibitory activity against proteases. The protease inhibitor cDNA was homologous to cDNA encoding a similar squirrel protein designated
                                                                                                                                                                                                                                                                                                                                                                                                                                      protease(s)
Claim 4; Page 8-9; 10pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KOND/) KONDO J.
(KANA-) ZH KANAGAWA KAGAKU
WPI; 97-369473/34.
                                                                                                                                                                                                                                                                         hibernation-related protein (HP-55). Sequence 413 AA;
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04-DEC-1995; 315692.
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larity 45.8%;
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372..381
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High-affinity melatonin receptor.

Melatonin receptor; G-protein-coupled receptor; glycosylation;
Melatonin receptor; G-protein-coupled receptor; glycosylation;
disulfide bond; ligand binding pocket; phosphorylation;
cytochrome-c family heme binding site; melatonin receptor-agonist;
melatonin receptor-antagonist; circadian rhythm disorder; jet-lag;
day-night cycle disorder; ovulation; reproductive cycle; antibody;
animal breeding; puberty; transgenic animal; drug screening.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 19; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-DEC-1995.
07-JUN-1995; U07360.
17-JUN-1994; US-261857.
07-OCT-1994; US-319887.
06-JUN-1995; US-319887.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LT 10
R13838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding high affinity melatonin receptor one - used to identify receptor agonists or antagonists e.g. for regulating circadian rhythm disorders or reproductive cycles claim 5; Fig 1; 115pp; English.
                                                                                                                                                                                                                                      (SUNR) SUNTORY LTD.
(DAIK) DAIKIN IND LTD.
Shibano Y, Toyoda H, Utsumi
WPI; 91-261442/36.
                                                                       The sequence was deduced from a clone isolated from a gene library prepd. from P. cepacia. It is the 1st of five proteins encoded by ORFs fadh-fadE which are essential for fusaric acid resistance. The protein has a mol. wt. of 47 kD. The genes can be introduced
                                                                                                                                                                                                                                                                                                                 04-SEP-1991
28-FEB-1991; 103006.
28-FEB-1990; JP-045481.
18-FEB-1991; JP-044027.
                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas cepacia, strain UK-1.
EP-444664-A.
                 disease caused by Fusarium fungi.
See also R13839-R13845.
                                                    The protein has a mol. wt. of 47 kD. The geneento plants in order to control plant diseases
                                                                                                                             Claim 18; Fig 4; 38pp; English.
The sequence was deduced from a
                                                                                                                                                                                                       N-PSDB; Q13369.
Fusaric acid re
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e.g. Pseud
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Best Local S
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Best Local Similarity
Matches 16; Conser
                                                                                                                                                                                                                                                                                                                                    12-DEC-1989; 100871.
13-DEC-1988; US-284119.
(COLS) UNIV COLORADO STATE R
(HARD) UNIV HARVARD.
HOOVEY EA, Mullins JI;
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This is the amino acid sequence of the barnacle (Megabalanus rosa) adhesion protein. The corresp. gene was isolated from a cDNA library using the probe T05723 which is derived from amino acid sequencing of the purified protein. The gene is used to produce an adhesive protein which can be used in water.
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R85478
R85478;
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ANALY STANDARD; Protein; 1784 AA.

R94427;

R94427;

11-JUN-1996 (first entry)

FELV F6A provirus clone 61E encoded nucleocapsid FeLV; retrovirus; vaccine; AIDS; disease model; iviraemia; leukaemia; therapy; nucleocapsid.

Feline immunodeficiency virus subtype A.

Feline immunodeficiency virus subtype A.
Inactivated FeLY-A sub-type isolates for use in disease vaccines - can be used to study prophylaxis and therapy immuno-deficiencies in other species, e.g. human. Disclosure; Fig 1; 22pp; English.
The nucleocapsid protein (R94427) and envelope protein sequences of felline leukaemia virus provirus F6A clone (deduced from open reading frames identified in the provided protein sequences.
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J07265081-A.
17-OCT-1995.
                                                                                                                                                                                                                                                                            WPI; 96-180826/19.
N-PSDB; T13265.
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06-MAR-1996.
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(KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO
WPI; 95-388699/50.
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Local Similarity 24.2%;
nes 23; Conservative
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5.64e+01;
-as 37;
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5.64e+01
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otein (R94428)
Hone 61E were
proviral DNA
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Best Local :
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Best Local
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30-APR-1993; E01063.
30-APR-1992; US-875940.
14-AUG-1992; US-929206.
17-SEP-1992; FR-001098.
16-APR-1993; FR-004545.
(ASSI-) ASSISTANCE PUBLIQUE.
(INSP) INST PASTEUR.
(MEDI-) MEDICAL RES COUNCIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (T13265). Clone 61E is replication competent and capable of inducing persistent viraemia in cats. Host cells, e.g. feline cell can be transformed with DNA derived from 61E and used to produce infectious virus useful in vaccines, in the generation of viraemia and in disease challenge systems.

Sequence 1784 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M.tuberculosis small ribosomal subunit S12 protein fragment. streptomycin; antibiotic; susceptibility; sensitive; resistar rpsL; mutant; small ribosomal subunit; S12 ribosomal protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding virus-A sub:type - producing AIDS type disease in cats, used to test drugs and vaccines.
Claim 6; Fig 1.1-17; 23pp; English.
Variant of viral genome induces immunodefficiency in cats similar NAIDS. May be used in research, especially in testing drugs and vaccines against vireamia and and feline leukaemia viruses.
Sequence 1784 AA;
                                    (UYBE-) UNIV BERNE.
(UYPA-) UNIY CURIE PARIS VI P & M.
GUYPA-) COLE S., Heym B, Honor
Young D, Zhang Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09322454-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1042 lafenirka-llsspalglpditkpfelfi 1070
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Hoover EA, Mullins JI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-JUL-1990.
12-DEC-1989; 122964.
13-DEC-1988; US-284139.
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R05898;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   687 LNYERARRPGLIGASVLGLDDIHRAWRTFV 716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90-218326/29.
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Similarity 36.7%;
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Pred. No. 7
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                                                                                 Honore N,
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7.72e+01;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Matches 1
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Example 2; Fig 14; 97pp; English.

The rpsL gene of M.leprae encodes the S12 protein of the small ribosomal subunit that is responsible for resistance to streptomycin. Two primers were designed based on this sequence and were used in a PCR amplification of M.tuberculosis DNA. Sequence analysis of the 306bp amplified fragment showed 28 differences between the rpsL gene from M.leprae (051533) and M.tuberculosis (061454). In streptomycin resistant strains, a single amino acid substitution due to a mutation in codon 43 (wild-type AAG mutated to AGG) was identified; substitution of Lys42 by Arg results in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-DEC-1992; 311622.

18-DEC-1991; US-811421.

(NEWE ) NEW ENGLAND BIOLABS

COMD DG, Jack WE, Kucera F

WPI; 93-198889/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA polymerase; intron; translation; bacteriophage NEB #619; E. mutation; cell growth; endonuclease; self splicing; stability; expression; transformation; expression vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R38095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant thermostable DNA polymerase from archaebacteria expressed efficiently by removal of intervening introns Claim 1; Fig 19; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rapid detection of antibiotic resistance in Mycobacteria isoniazid, rifampicin or streptomycin resistance in tuber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; Q43515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; Q61454
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T. litoralis DNA polymerase.
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Query Match Best Local

y Match 3.9%; Local Similarity 28.6%; hes 22; Conservative

Score Pred. 19; M

re 86; DB 8; Len d. No. 1.05e+02; Mismatches 28;

Length 1702 Indels

8

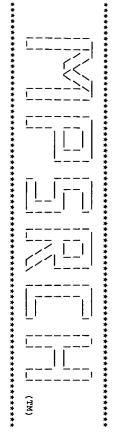
Gaps

7;

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- δð 1132 dgklvwkpvpyvmrhra 1148 : |: :|:|| 708 IHR-AWRT--FVLRVRA 721

Search completed: Fri Dec 18 18:35:58 1998 Job time : 59 secs.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Fri Dec 18 18:36:16 1998; MasPar time 12.67 Seconds 811.235 Million cell updates/sec

Description: Perfect Score: Sequence: Title:

>US-08-951-733-14 (640-940) from US08951733.pep (2 of 2) 2214

TSRLRFIPKPDGLRPIVNMD......NLRKTVVNFPVEDEALGGTA 301

Scoring table: PAM 150 Gap 11

Searched:

107076 seqs, 34141958 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: pir56 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 47.293; Variance 102.661; scale 0.461

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

222118 2322118 2322118	Result
99999999999999999999999999999999999999	Score
04444444444444444444444444444444444444	% Query Match
884 -94 -366 -189 -891 -891 -891 -891 -891 -189 -189	Length
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S53396 H70127 A64743 S49743 G64875 B46642 S58504 S58503 S58503 S58707 GNWYY A64767 A64767 S25023 S66771 S25023 S66771 S19381 S68700 S68700 S68700 S68700 S68701	ID
hypothetical protein hypothetical protein diff-binding protein hypothetical protein hypothetical protein aconitate hydratase (aconitate hydratase (aconitate hydratase (hypothetical protein reverse transcriptase serine chemoreceptor hypothetical protein genome polyprotein - genome polyprotein - genome polyprotein - genome protein on eurofilament-like pr hypothetical protein L-asparaginase I - Me oxi3 intron 2 protein	Description
1.84e-06 3.12e-01 1.20e+00 1.20e+00 1.57e+00 2.04e+00 2.04e+00 2.04e+00 3.43e+00 3.43e+00 3.43e+00 3.43e+00 3.43e+00 7.38e+00 7.38e+00 7.38e+00 7.38e+00 7.38e+00	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24
91	91	91	91	91	91	91	91	91	91	91	93	94	92	93	93	92	93	93	93	92	96
4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.2	4.2		4.2	4.2			4.2	4.2		4.3
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F69195	OKBYN2	HJNVAV	I56333	A31070	-C28821	F64045	S56487	ADSPAC	F69117	CFXCA	S03701	E64222	E64170	G70189	A53467	A69873	S45346	I51247	F65076	S73466	S17995
cell surface glycopro	protein kinase GCN2 (helicase (EC 3.6.1)	apolipoprotein B - ra	6-phosphofructokinase	1-phosphatidylinosito	excinuclease ABC, cha	hypothetical 40.4K pr	fructose-bisphosphate	conserved hypothetica	C-phycoerythrin alpha	141K protein - pea ea	topoisomerase IV chai	hypothetical protein	threoninetRNA ligas	protein kinase SNF1 h	phosphate starvation	fructose-bisphosphate	aldolase C - African	hypothetical protein	mble DNA primas	gene COX1 intron 1 pr
2.54e+01	2.54e+01	2.54e+0	2.54e+01	2.54e+0	2.54e+01	2.54e+01	2.54e+01	2.54e+01	2.54e+01	2.54e+01	1.56e+01	1.22e+01	1.99e+01	1.56e+01	1.56e+01	1.99e+01	1.56e+01	1.56e+01	1.56e+01	1.99e+01	7.38e+00

Qy	D	Qy	рb	Qy	Дb	Qy	DЬ	Qy	В	Д Ве	SUMMARY		GENE				#	**		REFE	ACCE	DATE	ORGA	ALTE	TITLE	ENTRY	RESULT	
918 CVVNLRKTV-VNFPVEDEAL 936	698 AKANRDKILAVSSQSDDDTV 717	861 TLLCSLCYGDM-E-NKLF-AGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYG 917	638 APIVDLVYDDLLEFYSEFKASPSQDTLILKLADDFLIISTDQQQVINIKKLAMGGFQKYN 697	801 HLQETSPLRDAVVIEQSSSLNEASSGLEDVFLRFMCHHAVRIRGKSVVQCQGIPQGSILS 860	593 NVR-TVHLSNQDVINVV-EM-EIF-K-TALWVEDKCYIREDGLFQGSSLS 637	743 PQ-DRLTEVIASIIKPONTYCVR-RYAVVOKAAHGHVRKAFKSHVSTLTDLQPYMRQFVA 800	539 PRMECMR-ILKDALKNENGFFVRSQY-FFNTNT-G-VLKLFNV-VNASRVPKPY-ELYID 592	686 VLNYERARRPGLIGASVIGIDDI-HRAWRTFVLRV-RA-QDPPPELYFVKVDVTGAYDTI 742	481 ILEYLRNKRPTSF-TKIYSPTQIADRI-KEFKQRLLKKFNNVLPELYFMKFDVKSCYDSI 538	Query Match 6.7%; Score 148; DB 2; Length 884; Best Local Similarity 26.2%; Pred. No. 1.84e-06; Matches 68; Conservative 67; Mismatches 93; Indels 32; Gaps 25;	#MARY #length 884 #molecular-weight 102662 #checksum 7604	#gene SGD:ESTZ ##cross-references SGD:S0004310; MIPS:YLR318w	GENETICS	##experimental_source strain S288C (AB972)	##DESIQUES I-884 ##LADEL DUZ	_type	S53396 °	n The sequence	#submission submitted to the EMBL Data Library, February 1995		S S	U5-May-1995 #sequence_revision O1-Sep-1995 #cexc_cmange	NISM #formal_name Saccharomyces cer	ALTERNATE_NAMES hypothetical protein L8543.12	hypothetica	S53396 #type complete		ALIGNMENTS

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Best Local Similarity 26.8%;
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                                                                                                        #cross-references
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##molecule_type DNA
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#molecular-weight 10659
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                                                                                                                                          Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.;
Sutton, G.G.; Fleischmann, R.D.; Ketchum, K.A.; Klenk,
H.P.; Gill, S.; Dougherty, B.A.; Nelson, K.; Quackenbush,
J.; Zhou, L.; Kirkness, E.F.; Peterson, S.; Loftus, B.;
Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.;
McKenney, K.; Fitzegerald, L.M.; Lee, N.; Adams, M.D.;
Hickey, E.K.; Berg, D.E.; Gocayne, J.D.; Utterback, T.R.;
Peterson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.;
Fujii, C.; Bowman, C.; Watthey, L.; Wallin, E.; Hayes,
W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
C.M.; Venter, J.C.
Nature (1997) 388:539-547
The complete genome sequence of the gastric pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTP-binding protein Helicobact #formal_name Helicobacter pylori 09-Aug-1997 #sequence_revision 0
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                                                                              A64591
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burgdorferi.
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s MUID:97394467
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                          preliminary; nucleic acid sequence not shown;
translation not shown
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g protein - Helicobacter pylori (strain 26695)
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Pred. No. 3.12e-01;
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19; Mismatches 30;
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##cross-references GB:AE000571; G:
TIGR:HP0569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      732 KVDVTGAYDTIPQDRLTEVIASIIKPQN 759
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      757
##experimental_source strain K-12, substrain MG1655
                                                                       ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             673 AERLTSRV-KALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFV 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##cross-references EMBL:246659; NID:g575680; PID:g575683; MIPS:YML036w
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                                  ##cross-references GB:AE000225; GB:U00096; NID:g1787523; PID:g1787531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 GEOMYSAIYKTLIEV-KYNKMRTRNLNSECVLCLSPTSNISDAF-LKFGIKDDSSQLICL 107
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Similarity 25.8%;
16; Conservation
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Similarity 26.1%;
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aconitate hydratase (EC 4.2.1.3) - Escherichia coli
#formal_name Escherichia coli
12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change
05-pec-1997
                                                                                                               G64875
                                                                                                                                                                     Science (1997) 277:1453-1462
                                                                                                                                                                                                      Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Kiley, M.; Collado-Vides, J.; Glasner, J.D.; Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to S49743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #formal_name Saccharomyces cerevisiae
13-Jan-1995 #sequence_revision 10-Feb
21-Nov-1997
                                                                                                                                                                                                                                                                                                  G64875; S22375; A49756
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                                                                                            nucleic acid sequence not shown;
                                                       1-891 ##label BLAT
                   UWGP: b1276
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Pred. No. 1.
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21; Mismatches
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Pred. No. 3.12e-01
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##residues 'X',3-15,'X',17,'X',19 ##label
                                                                                                        ##molecule_type DNA
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Local Similarity 21.9%;
nes 14; Conservative
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J. Bacteriol. (1993) 175:5666-5676

The major iron-containing protein of Legionella pneumophila
is an aconitase homologous with the human iron-responsive
element-binding protein.
                                                                                                                                                                                                                                                                                                            B48642 #type complete
aconitate hydratase (EC 4.2.1.3) - Legionella pneumophila
#formal_name Legionella pneumophila
03-May-1994 #sequence_revision 03-May-1994 #text_change
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The aconitase of Escherichia coli: purification and molecular cloning and map location of the
                                                                                                                                                B48642
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Eur. J. Biochem. (1992) 204:599-609
The aconitase of Escherichia coli. Nucleotide sequence of
aconitase gene and amino acid sequence similarity with
mitochondrial aconitases, the
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binding_site 4Fe-4S cluster (Cys) (covalent) #status
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 Score 103;
 DB
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the nucleotide sequence was submitted to the EMBL Dat
##note Library, February 1994
RY #length 205 #molecular-weight 23260 #checksum 7617
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##note the nucleotide sequence was submitted to
Library, April 1995
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##residues 1-205 ##label ESP
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                                                                                                                                                                                                                                                                                                                              GLRPIVNMDYV-VGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVL-GLDDI
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Similarity 22.1%;
33; Conservative
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                            $58503 #type fragment reverse transcriptase like protein 1, introduced alga (Pylaleila littoralis) (fragment) #formal_name Pylaleila littoralis 29-Nov-1995 #sequence_revision 01-Mar-1996 01-Mar-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       site-specific excision.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S72329
Esposito, D.; Scocca, J.J.
Mol. Microbiol. (1994) 13:685-695
Identification of an HPl phage protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #formal_name phage HP1
#formal_name phage HP1
06-Dec-1996 #sequence_revision 13-Mar-1997
31-Oct-1997
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                                                                                                                                                                                                                                                                                                                                                                                             Score 102; DB 2; Le Pred. No. 1.57e+00; 49; Mismatches 50;
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22; Mismatches 23;
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#title
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#authors Boyd, A.; Kendall, K.; Simon, M.I.
#journal Nature (1983) 301:623-626
#title Structure of the serine chemorecep
#cross-references MUID:83141753
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##cesidues 1-503,'x',505-551 ##label BUR
##cross-references EMBL:U14003; NID:g1263172; PID:g537197
##note the nucleotide sequence was submitted to the j
##note Library, August 1994
                                 ##molecule_type DNA
#residues 1-147,'STSSLISRPRDIRN',162-536 ##label
##cross-references GB:V00373; GB:J01718; NID:g43217; PI
NCE $30279
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##residues 1-55
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Similarity 46.7%;
14; Conservative
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J. Mol. Biol. (1995) 251:378-389
The mitochondrial LSU rDNA of the brown alga Pylaiella
littoralis reveals alpha-proteobacterial features and is
split by four group IIB introns with an atypical phylogeny.
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The complete genome sequence of Escherichia
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methyl-accepting chemotaxis protein I (MCP-I)
#formal_name Escherichia coli
14-Nov-1983 #sequence_revision 13-Feb-1998 #text_change
Roper, D.I.; Fawcett, T.; Cooper, R Mol. Gen. Genet. (1993) 237:241-250
                                                                                                                                                                                                                                                                                                                                                                                                                     Analysis of the Escherichia coli genome VI: the region from 92.8 through 100 minutes.
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                                                                                                                       A03442
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th 318 #checksum 7326
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Pred. No. 1.57e+00;
7; Mismatches 8;
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Best Local
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                                                                                                     #journal
#title
                   #cross-references MUID:87218532
#accession $20168
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##cross-references GB:S56952; NID:g298654; PID:g298656
##cross-references GB:S56952; NID:g298654; PID:g298656

This protein responds to changes in serine concentration in the environment, transduces a signal from the outside to the inside of the cell, and facilitates sensory adaptation through various levels of methylation.
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##residues 1-7
                                                                                                                                                                  ##cross-references EMBL:X05143; NID:g4019; PID:g4020
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                                                                                                                                                                                                       ##molecule_type DNA
##residues 1-184 ##label SLO
                                                                                                                                                                                                                                                                                                                                                      ##molecule_type DNA
##residues 1-1114 ##label
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                                                                                                                                                                                                                                                                                                             ##cross-references EMBL:U19104; NID:g609423; PID:g609425; MIPS:YLR383w
NCE $15581 .
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Similarity 22.48;
22; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein L3502.2
#formal_name Saccharomyces cerevisiae
23-Feb-1995 #sequence_revision 12-May-1995
                                                        Labouesse, M.; Herbert, C.J.; Dujardin, G.; Slonimski, P.I
EMBO J. (1987) 6:713-721
Three suppressor mutations which cure a mitochondrial RNA
maturase deficiency occur at the same codon in the open
reading frame of the nuclear NAM2 gene.
                                                                                                                                                                                                                                                submitted to the EMBL Data $20170
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chemotaxis; methylated amino acid; sensory transduction;
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#modified_site glutamate methyl
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#modified_site glutamate methyl ester
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cheB-dependent deamidation and methylation) #status
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Pred. No. 2.04e+00;
28; Mismatches 4;
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1133-1151
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#journal Mol. Gen. Genet. (1988) 213:297-309
#title Divergence of the mitochondrial leucyl tRNA synthetase genes
in two colosely related yeasts Saccharomyces cerevisiae and
Saccharomyces douglasii: a paradigm of incipient evolution.
#cross-references_MUID:89039717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##status nucleic acid sequence not shown; translation not shown ##molecule_type genomic RNA | 1-3411 ##label DUP | 1-3411 ##label DUP
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Local Similarity 40.8%;
hes 20; Conservative
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Nucleotide sequence comparison of the genome of two 17D-204

yellow fever vaccines.

nces MUID:89282413

S07757
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E; nonstructural protein NS1; nonstructural protein NS2a;
nonstructural protein NS2b; nonstructural protein NS3;
nonstructural protein NS4a; nonstructural protein NS4b;
nonstructural protein NS5
#formal_name yellow fever virus
31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change
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#product major envelope protein E #status predicted
#label MEE\
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#domain transmembrane *status predicted *label TMI\
#product envelope protein M *status predicted *label
                         #domain transmembrane #status predicted #label TM5\
#domain transmembrane #status predicted #label TM6\
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product nonstructural protein NS2a #status predicted
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1355-1484	1159-1180 1188-1354	740-753 755-778 779-1187	249-269 271-285 286-778	FEATURE 2-210 211-285	#accession ##molecule_ ##residues LASSIFICATION EYWORDS	journal title	ACCESSIONS REFERENCE #authors	ORGANISM DATE	RESULT 12 ENTRY TITLE CONTAINS	Qy 885 LLRLV 889	Db 1392 LMMLV 1	Db 1334 GLTQPFLG-LCAFL : : Qy 826 GLFDVFLRFMCHH-	Query Match Best Local Simi Matches 21;	SUMMARY	134,150,172,594, 908,986,1796,2062, 2320,2346,2408, 2467,2720,2734, 2740	2507-3411	2395-2506	2108-2394	1485-2107	1355-1484
#product nonstructural protein NS2b #status predicted	#domain transmembrane #status predicted #label TM5\ #product nonstructural protein NS2a #status predicted	#domain transmembrane #status predicted #label TM3\ #domain transmembrane #status predicted #label TM4\ #product nonstructural protein NS1 #status predicted #label NG1V	#domain transmembrane #status predicted #label TM1\ #domain transmembrane #status predicted #label TM2\ #product major envelope protein E #status predicted #label MEE\	722	A03914 A03914 Ltype genomic RNA Ltype genomic RNA 1-3411 ##label RIC #superfamily yellow fever virus genome polyprotein capsid protein; envelope protein; glycoprotein; nonstructural protein; polyprotein; transmembrane protein	ence leoti laviv	A03914 A03914 Rice, C.M.; Lenches, E.M.; Eddy, S.R.; Shin, S.J.; Sheets, R.L.: Strauss, J.H.	#formal_name yellow fever virus 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 12-Apr-1996	GNWVY #type complete genome polyprotein - yellow fever virus (strain 17D) genome polyprotein C; envelope protein M; major envelope protein E; nonstructural protein NS1; nonstructural protein NS2a; nonstructural protein NS2b; nonstructural protein NS3; nonstructural protein NS4a; nonstructural protein NS4b; nonstructural protein NS4a; nonstructural protein NS4b;	39	1396	3-LCAFLATRIFGRRSIPVNEALAAAGLVGVLAGLAFQEMEN-FLGPIAVGGL 1391 	4.6%; Score 101; DB 1; Length 3411; larity 32.3%; Pred. No. 2.04e+00; Conservative 14; Mismatches 27; Indels 3; Gaps 3;	predicted th 3411 #molecular-weight	#	# rade: N45\ #product nonstructural protein NS5 #status predicted #label NS5\		NS3\ nonstructural	N2B\ nonstructural protein NS3 #status p	•

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KEYWORDS acyltransferase
SUMMARY #length 372 #moloc
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Best Local Similarity 34.0%;
Matches 18; Conservative
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594,755,908,986,
1796,2062,2320,
2346,2408,2467,
2720,2734,2740
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                                                                                                                                                                                                 ##molecule_type DNA
##residues 1-372 ##label BUL
##cross-references GB:U67570; GB:L77117; NID:g1591929; PID:g1591936;
##cross-references GB:MJ1298; PID:g1511307
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  729
                          296 YEFIKEDNLTPIYPFIFKEKTMEIAEHLIK-NNIFCVGIRYPTVPKGLE-RIR 346
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  Y-FVKVD-VTGAYDTIPQDRLTEVIASIIKPQNTYCV-RRYAVVQKAAHGHVR 778
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Similarity 32.3%;
21; Conservative
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Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.
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Pred. No. 3.43e+00;
11; Mismatches 19
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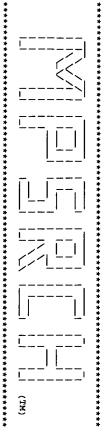
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                                                                                                                                                          SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
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#accession
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                                                                                                                                                                                                                                                                                             #submission
                                                                                                                                                                                                                                                                                                                 authors
                                                                                                                                                                                              ##molecule_type mRNA
##residues 1-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##residues 1-446 ##label HAR ##residues 1-446 ##label HAR
  642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   315 AELVTGFRDVAS-ETRVVLDVDPEVEGSSPGELAELSIYRF 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        676 LTSRVKALFSVLNYERARRPGLIGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDV 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          203 LAAGVNALASHLQAEQAEN-DLLQARLIGSSEAERS-R-IALDLH-DEMGPQLFALRAAV 258 | : | : | : | : | : | : : : | : | : : : |
                                                                                                                                                    ##rcsidus 1-57 ##label ADJ
##cross-references EMBL:X66695; NID:g9511; PID:g9512
# #length 557 #molecular-weight 62921 #ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            736 TGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYM 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                259 SHA-QAMTAD-LPERPAALDETLDAIAGHALEV-QRSARTAI-NDLRPMLLGEASLAELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##molecule_type DNA
                                                                                                                                                                                                                                      ##status
                                      33 RIKMFMPRAYELKVTVIKMAFELSTRCSKRDGVVETVLTDVIEGK-TMSGYDRSGRVNLL
                                                                                            Match 4.5%;
Local Similarity 25.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14
  RLR-FIPKPDGLR-PIVNMDYVVGARTFRREKRAER-LTSRVKALFSVLNYERARRPGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RQFVAHLQETSPLRDAVVIEQSSSLNEASSG-LFDVFL-RF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 4.5%;
similarity 21.7%;
35; Conservative
                                                                                                                                                                                                                                                    Adjaye, J.A.; Eagles, P.A.M. submitted to the EMBL Data Library, June 1992 Cloning of a novel neurofilanment like protein $25023
                                                                                                                                                                                                                                                                                                                                                                                                                             $25023 *type complete neurofilament-like protein - northern European squid *formal_name Loligo forbesi *common_name northern European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #formal_name Paracoccus denitrificans
31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
09-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                       20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
  09-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S3287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transmembrane protein
#length 446 #molecular-weight 48236 #checksum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identification of a two-component regulatory system controlling methanol dehydrogenase synthesis in Paracoccus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mol. Microbiol. (1993) 8:457-470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Harms, N.; Reijnders, W.N.M.; Anazawa, H.; van der Palen, C.J.N.M.; van Spanning, R.J.M.; Oltmann, L.F.; Stouthamer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                regulatory protein moxY -
                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 99; DB 2; I
Pred. No. 3.43e+00;
55; Mismatches 60
                                                                          Score 100; DB 2; Le
Pred. No. 2.65e+00;
21; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Paracoccus denitrificans
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                                                                                                                                                                                                                                                                        protein
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                                        91
                                                                              4
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Dec 18 18:37:17 1998; MasPar time 9.66 Seconds 836.466 Million cell updates/sec

Tabular output not generated.

Title:

Description: Perfect Score: Sequence: >US-08-951-733-14 (640-940) from US08951733.pep (2 of 2) 2214

TSRLRFIPKPDGLRPIVNMD......NLRKTVVNFPVEDEALGGTA 301

Scoring table: PAM 150 Gap 11

Searched: 74019 seqs, 26840295 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

swiss-prot35 1:swissprot

Statistics: Mean 49.063; Variance 85.433; scale 0.574

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

2222221 1 1 5 6 6 6 6 7 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7	Result No.
100 100 100 100 100 100 100 100 100 100	Score
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1890 890 205 551 1114 446 1938 1030 586 1238 362 2138 2138 2138 2138 2138 2138 2147 2147 2147 2147 2147 2147 2147 2147	
	B
YMD6_YEAST ACOL_ECOLI ACON_LEGPN YOO1_BPHP1 MCP1_ECOLI RH18_YEAST POLG_YEFV1 POLG_YEFV2 POLG_YEFV2 MOXY_PARDE YEB02_SCHPO YCF1_YEAST ACON_BRAJA ACON_BRAJA ACON_BRAJA ACON_BRAJA ACON_BRAJA ACON_BRAJA ACON_BRAJA ACON_BRAJA ACON_BRAJA ACON_BRAJA ACON_BRAJA ACON_BRAJA ACON_BRAJA ACON_BRAJA ACON_BRAJA ACON_BRAJA ACON_BRAJA ACON_BRAJA ACON_BRAJA YEAST YO10_MYCEN YAGE_ECOLI YAGE_ECOLI YAGE_ECOLI YAGE_ECOLI PARC_MYCGE PHSC_YEAST	ID
ACONITATE HYDRATASE 1 ACONITATE HYDRATASE (E HYPOTHETICAL 23.2 KD P METHYL-ACCEPTING CHEMO DNA REPAIR PROTEIN RHC GENOME POLYPROTEIN (CO METHANOL UTILIZATION C PUTATIVE HELICASE C17H HYPOTHETICAL 55.1 KD P ACONITATE HYDRATASE (E PROTEIN TYROSINE PHOSP CAPSID PROTEIN VP23 FRICTOSSE-BISPHOSPHATE PROBABLE L-ASPARAGINAS PUTATIVE COX1/OXI3 INT HYPOTHETICAL PROTEIN HYPOTHETICAL PROT	Description
1.00e-01 2.00e-01 2.00e-01 3.76e-01 3.76e-01 3.76e-01 3.76e-01 3.76e-01 3.76e-01 3.76e-01 7.00e-01 7.0	Pred. No.

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88888	99999999	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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127 133 532 957	452 609 695 780 1475 1590	1117 124 164 297 309 357 366 428 428
		4444444
TRM8_ECOLI RR12_CHLRE RTCR_ECOLI NIRB_KLEPN	YHA2_YEAST UVRC_HAEIN PIP6_BOVIN K6PL_MOUSE TRA2_CAEEL GCN2_YEAST RR12_HORVU	YDVG_SCHPO RR12_EUGGR RPHEA_FREDI YOXG_BACSU VIRB_SHIFL ALF_SPIOL ALF_SPIOL YJGP_ECOLI MILC_XENLA DDI1_YEAST FUSA_BURGE LAFB_VIRBGE
	HYDOTHETICAL 51.2 KD B EXCINGLEASE ABC SUBUN 1-PHOSPHOFRUCTOKINASE, 6-PHOSPHOFRUCTOKINASE, SEX-DETERMINING TRANSF PROTEIN KINASE GCN2 (E CHLOROPLAST 30S RIBOSO	PUTATIVE HELICASE C6F1 CHLOROPLAST 30S RIBOSO C-PHYCOERYTHRIN ALPHA HYPOTHETICAL 32.5 KD P VIGULENCE REGGLON TRAN FRUCTOSE-BISPHOSPHATE HYPOTHETICAL 40.4 KD P MELATONIN RECEPTOR TYP DNA-DAMAGE INDUCIBLE P FUSARIC ACID RESISTANC ETAGETIAN HONE ASSOTTANC ETAGETANCH HONE HONE ASSOTTANC ETAGETANCH HONE ASSOTTANCH HONE ASSOTTANCH HONE HONE ASSOTTANCH HONE HONE HONE ASSOTTANCH HONE HONE HONE HONE HONE HONE HONE HON
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ALIGNMENTS

RRRCC	SSS		급	92	38	RESULT	Qy	Db	Qy	망	M B Q	QS	ΚW	S 2	2 2	RC	RP	R C	S	GN	DE	ğ	3 13	AC	RESULT ID Y	1
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; ENTEROBACTERIACEAE. [1] SEQUENCE FROM N.A. MEDLINE; 92174916.	COLI.	YDRATAS	(REL. 22,	01-MAY-1992 (REL. 22, CREATED)	ACO1_ECOLI STANDARD; PRT; 890 AA.	ω	732 KVDVTGAYDTIPQDRLTEVIASIIKPQN 759	108 KFH-TNT-DDVDKEQLRTIMTSIVKGQE 133		50 GEQMYSAIYKTLIEV-KYNKMRTRNLNSECVLCLSPTSNISDAF-LKFGIKDDSSQLICL 107	Query Match 4.7%; Score 103; DB 1; Length 181; Best Local Similarity 26.1%; Pred. No. 2.00e-01; Matches 23; Conservative 25; Mismatches 35; Indels 5; Gaps 5;	SEQUENCE 181 AA; 20662 MW; AC111C34 CRC32;	ICAL PROTEIN.	SUBMITTED (NOV-1994) TO EMBL/GENEANN/DDBG DATA BANNS: EMBL: Z46659: G575683: ALT_SEQ.	BADCOCK K., CHURCHER C., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;	288C / AB972;	SEQUENCE FROM N.A.	EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.	SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).		L 20.7 KD P	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)	(REL. 35,		LT 1 YMD6_YEAST STANDARD; PRT; 181 AA.	

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RESULT
AC PODT OUT
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Best Local Similarity 21.9%;
Matches 14; Conservative
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SEQUENCE
                                                                P37032;
01-JUN-1994 (REL. 29, CREATED)
01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
01-JUN-1994 (REL. 29, LAST ANNOMATION UPDATE)
ACONITATE HYDRATASE (EC 4.2.1.3) (CITRATE HYDRO-LYASE) (ACONITASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; S223
ECOGENE;
PROSITE;
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AIBA H., BI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE000225; G1787531; -.
EMBL; D90765; G1742087; -.
EMBL; D90766; G1742090; -.
EMBL; S22375; S22375.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AIBA H., BABA T., FUJITA K., HAYASHI K., HONJO A., HORIUCHI T., IKEMOTO K., INADA T., ISONO K., ISONO S., ITOH T., KANAI K., KASAI H., KASHIMOTO K., KIM S., KIMURA S., KITAGAMA M., KITAKAWA M., MAKINO K., MASUDA S., MIKI T., MIZOBUCHI K., MORI MOTOWIRA K., NAKAMURA Y., NASHIMOTO H., NISHIO Y., OSHIMA T., SAITO N., SAMPEI G., SEKI Y., TAGAMI H., TAKEMOTO K., WADA C., YAMAMOTO Y., YANO M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BLATTNER F.R., PLUNKETT SUBMITTED (JAN-1997) TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-K12 / MG1655;
BLATTNER F.R., PLUNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X60293; G40896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRODROMOU C., ARTYMIUK P.J., GUEST J.R.; EUR. J. BIOCHEM. 204:599-609(1992).
  LEGIONELLA PNEUMOPHILA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBMITTED (DEC-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-18
                                             MAJOR IRON-CONTAINING PROTEIN) (MICP) (IP210)
                                                                                                                                                                                                                                                                                703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERCONVERTS CITRATE, CIS-ACONITASE, AND SIMILARITY: BELONGS TO THE ACONITASE/IPM
                                                                                                                                                                                                                                                                             TGLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ps00450; ACONITASE_1; 1.
ps01244; ACONITASE_2; 1.
TRICARBOXYLIC ACID CYCLE; IRON-SULFUR; 4FE-4S.
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                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             521 ,
97516 MW;
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EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 105;
Pred. No. 1.
22; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BY SIMILARITY).
G -> S (IN REF. 2).
; 276673F6 CRC32;
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(BY SIMILARITY).
IRON (IRON-SULFUR CLUSTER)
(BY SIMILARITY).
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                                                                                                                                                                                     PRT;
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.06e-01
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FEW MARK SOLUTION OF THE STATE 
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P SEQUENCE FROM N.A.

C STRAIN-PHILADELPHIA 1;

X MEDLINE; 93374864.

X MEDLINE; 93374864.

A MENGAUD J.M., HORWITZ M.A.;

A MENGAUD J.M., HORWITZ M.A.;

L J. BACTERIOL. 175:5666-5576(1993).

C -!- CATALYTIC ACTIVITY: CITRATE = CIS-ACONITATE + H(2)O.

C -!- PATHWAX: TRICARBOXYLIC ACID CYCLE.

C -!- SUBUNIT: MONOMER (BY SIMILARITY).

C -!- SUBUNIT: MONOMER (BY SIMILARITY).

C THE ACTIVE (4FE-4S) CLUSTER IS PART OF THE CATALYTIC SITE THA CONITACONIVER'S CITRATE, CIS-ACONITASE, AND ISOCITRATE.

C -!- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY.

R EMBL; L22081; G348945; -.

R PIR; B48642; B48642.
                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 4.78;
Best Local Similarity 25.08;
           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE;
ESPOSITO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YOO1_BPHP1 STANDARD; PRT; 205 AA. P51700; P51700; O1-OCT-1996 (REL. 34, CREATED) O1-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE) O1-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE) HYPOTHETICAL 23.2 KD PROTEIN IN INT-C1 INTERGENIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METAL
                                                                                                                                                                                   ESPOSITO D., FITZMAURICE W.P., BENJAMIN WALDMAN A.S., SCOCCA J.J.; WALDMAN A.S., SCOCCA J.J.; SCOCCA J.G.; SC
                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-HP1C1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00450; ACONITASE_1; 1.
PROSITE; PS01244; ACONITASE_2; 1.
LYASE; TRICARBOXYLIC ACID CYCLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI; LEGIONELLACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-HP1C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VIRIDAE; DS-DNA NONENVELOPED VIRUSES; MYOVIRIDAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BACTERIOPHAGE HP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISSP; P20004; 1ACO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  755 MRYQENQQDLYIIAGKEYGTGSSR-DWAAKGTNLLG-VKAVITE-SFERIHRSNLIGMGI 811
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MICROBIOL. 13:685-695(1994).
4.68;
Similarity 22.18;
33; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
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D., SCOCC
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                                                                                                                                                  205 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCOCCA J.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                  69 P
23260 MW;
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              49;
                                            Score 102; DB 1;
Pred. No. 2.75e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 103; DB 1;
Pred. No. 2.00e-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IRON (IRON-SULFUR CLUSTER)
(BY SIMILARITY).
IRON (IRON-SULFUR CLUSTER)
(BY SIMILARITY).
IRON (IRON-SULFUR CLUSTER)
                                                                                                                                                  POTENTIAL.
821C7A9F
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              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                 R.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRC32;
                                                                                                                                                      CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                        GOODMAN S.D.,
                                                                             Length 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 891
              Indels
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              17;
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       Gaps
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         C -I- FUNCTION: RECEPTOR FOR THE ATTRACTANT L-SERINE AND RELATED AMINO ACIDS AND IS ALSO RESPONSIBLE FOR CHEMOTAXIS AWAY FROM A WIDE RACEDS AND HEALTH SINCE FOR THE ACTURENT AND WEAK ACIDS.

C RANGE OF REPELLENTS, INCLUDING LEUCINE, INDOLE, AND WEAK ACIDS.

C PROCTION: CHEMOTACTIC-SIGNAL TRANSDUCERS RESPOND TO CHANGES IN THE CONCENTRATION OF ATTRACTANTS AND REPELLENTS IN THE ENVIRONMENT, THE CONCENTRATION OF ATTRACTANTS AND REPELLENTS IN THE ENVIRONMENT, AND FACTLITARE SENSORY ADAPTATION THROUGH THE VARIATION OF THE LEVEL OF METHYLATION ATTRACTANTS INCREASE THE LEVEL OF METHYLATION THE METHYL CROOPS ARE ADDED BY THE METHYLTRANSFERASE CHER AND REMOVED BY THE METHYLTRANSFERASE CHER AND REMOVED BY THE METHYLTRANSFERASE CHER AND REMOVED BY THE OTHER BACTERIAL CHEMOTAXIS SENSORY TRANSDUCERS.

C -I- SUBLICARTY: TO THE OTHER BACTERIAL CHEMOTAXIS SENSORY TRANSDUCERS.

DR EMBL; J01718; G148077; -.

EMBL; J01718; G33197; -.

REMBL; AE000506; G2367378; -.

REMBL; S56952; G298656; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P02942; P76817;
21-JUL-1986 (REL. (
01-JUL-1993 (REL. 2
15-JUL-1998 (REL. 3
                                                                                                                                                                                                                                                                                             T. BIOL. CHEM. 266:9746-9753(1991).
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 295-317 AND 483-507, AND MEDLINE; 82265699.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-K12 / MG1655;
MEDLINE; 95334362.
BURLAND V.D., PLUNKETT G. III, SOFIA H.J., DANIELS D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
STRAIN-K12 / MG16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE; 83141753.
BOYD A., KENDALL K., SIMO
NATURE 301:623-626(1983)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-77 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENTEROBACTERIACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESCHERICHIA COLI.
PROKARYOTA; GRACILICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               METHYL-ACCEPTING CHEMOTAXIS
                                                                                                                                                                                                                                                                                                                           POST-TRANSLATIONAL MEDLINE; 91236753.
                                                                                                                                                                                                                                                                                                                                                                                         KEHRY M.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOL. GEN. GENET. 237:241-250(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ROPER D.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 93204900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEIC ACIDS RES. 23:2105-2119(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BLATTNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       763
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                                                                                                                                                                                                                                                                                                                                                                         BIOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HRAWRITFVLRV-RAQDPP-PELY-FVKVDVTGAYDTIPQDRLTEVI-A-SIIKPQNTYC- 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -KEYNAIQLKIFWDIEHSLSTLYMFDKSN-KQEIDTILGYLLKDINSATSLIEKHARYDE 164
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                                                                                                                                                                                                                                                                                                                                                                           CHEM.
                                                                                                                                                                                                                                                                                                                                                                        DAHLQUIST F.W.;
EM. 257:10378-10386(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FAWCETT T., COOPER R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01, CREATED)
26, LAST SEQUENCE UPDATE)
36, LAST ANNOTATION UPDATE)
CHEMOTAXIS PROTEIN I (MCP-I)
                                                                                                                                                                                                                                                                                                                                             MODIFICATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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Best Local :
                                                                                                                           SEQUENCE FROM N.G.
STRAIN=S288C / AB972;
STRAIN=S288C / AB972;
JOHNSTON M., ANDREWS S., BRINKMAN R., COOPER J., LITTON J., KUCFAVELLO A., FULTON L., GATTUNG S., GRECO T., KIRSTEN J., KUCFAVELLO A., FULTON J., HILLIER L., JIER M., JOHNSON D., HALLSWORTH K., HAWKINS J., HILLIER L., LE T., MARDIS E., M'TOHNSTON L., LANGSTON Y., LATRETLLE P., LE T., MARDIS E., M'TOHNSTON L., LANGSTON D., RIFKEN L., RILES
                                                                                           JOHNSTON L., LANGSION ... PAULEY A., PELUS MILLER N., NHAN M., PAULEY A., PELUS TAICH A., TREVASKIS E., VIGNATI D., WATERSTON R., WATERSTON R.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOD_RES
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SEQUENCE
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DOMAIN
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ECO2DBASE; B060.4;
ECO2DBASE; B060.5;
                                                                                                                                                                                                                                                                                                            MEDLINE; 96069417.
LEHMANN A.R., WALICKA M., GRIFFITHS I
MCCLERADY S., CARR A.M.;
MOL. CELL. BIOL. 15:7067-7080(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ECOGENE; EG11034;
PROSITE; PS00538;
CHEMOTAXIS; TRANSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ECO2DBASE; B060.7;
ECO2DBASE; B060.8;
ECOGENE; EG11034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P02941;
ECO2DBASE; B0
                                      STRAIN-AB1-4A/8/55;
                                                            SEQUENCE OF 1-184 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ECO2DBASE; B060.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       795 MRQFVAHLQETSPLRDAVVIEQSSSLNEASSGLFDVFL 832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164 EKQYVAYMEQNDRLHDIAVSDNNASYSQAMWILVGVMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  737 GAYDTIPQD-RLTEVIASIIKPQ-NTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPY 794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 ADYEALPRDPRQSTAAAAEIKRNYDIYHNALAELIQLLGAGKINEFF-DQ-PTQGYQDGF 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
22; Conser
                      87218532
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191
211
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                                                                                                   EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ¥
                                                                                                                                                                                                                                                                                                                                                       GRIFFITHS D.J.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 101; DB 1;
Pred. No. 3.76e-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
THE 3 ARG MAY FORM A POSITIVELY CHARGED POCKET, WHICH BINDS THE ALPHA-CARBOXYL GROUP OF THE ATTRACTANT AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
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                                                                                                                                                                                                                 R., COOPER J., DING H., DU Z., GRECO T., KIRSTEN J., KUCABA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; 1.
METHYLATION; PERIPLASMIC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRC32;
                                                                                                                                                                                                                                                                                                                                                         MURRAY J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              201
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                                                                                                                                                                            MENEZES S.,
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HERBERT C.J.,

DUJADIN G., SLONIMSKI P.P.;

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SOOR FITTERS
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Best Local S
Matches 2
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21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 05, LAST ANNOTATION UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
GENOME POLYPROTEIN (CONTAINS: CAPSID PROTEIN CORE PROTEIN E; NONSTRUCTURAL PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEIN NS1, NS2B, NS4B AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48) (NS5)).
YELLOW FEVER VIRUS (STRAIN 17D).
VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; FLAVIVIRIDAE;
                      CHAIN
PROPEP
CHAIN
CHAIN
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                                                                                                                                                                                                                                                                                                                                               MEDLINE; 85
RICE C.M.,
 TRANSMEM TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
DOMAIN
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SCIENCE 229:726-733(1985).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
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                                                                                                                                                                                            PIR; A03914; GNWVY.
POLYPROTEIN; GLYCOPROTEIN;
                                                                                                                                                                                                                 PROTEIN M AND GLYCOPROTEIN E. THE PROTEIN C AND MRNA.
EMBL; X03700; G59339; -.
EMBL; K02749; G336193; -.
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE; 85272570.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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DNA REPAIR;
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                                                                                                                                                                        NONSTRUCTURAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45
                                                                                                                                                                                                                                                               FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRARE-RELATED FUNCTION. NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION. SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLECCAPSID COVERED BY LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _YEFV1
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 122
211
216
216
217
217
213
1131
1135
11485
2108
2257
249
                                                                                                                                                                                                                                                                                                                                             LENCHES E.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATP-BINDING; COILED COIL; NUCLEAR PROTEIN.
35 39 NUCLEAR LOCALIZATION SIGNAL
109 116 ATP (POTENTIAL).
259 529 COILED COIL (POTENTIAL).
696 969 COILED COIL (POTENTIAL).
1114 AA; 128008 MW; BC94F87E CRC32;
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                                                                                                                                                                      PROTEIN
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 121
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285
778
1130
1354
1484
1484
2107
2256
2506
2506
269
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                                                                                                                                                                                  PROTEIN;
                                                                                                                                                                                                                                                                                                                                             EDDY S.R., SHIN S.J.,
                                                                                                                                                                                 RNA-DIRECTED RNA POLYMERASE; TEIN; HELICASE; ATP-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 101; DB 1;
Pred. No. 3.76e-01;
                                                                ENVELOPE GLYCOPROTEIN M.
MAJOR ENVELOPE PROTEIN E.
NONSTRUCTURAL PROTEIN NS1.
NONSTRUCTURAL PROTEIN NS2A.
NONSTRUCTURAL PROTEIN NS2B.
                                 NONSTRUCTURAL NONSTRUCTURAL
                                                                                                                                                 REMOVED FROM CAPSID PROTEIN CELLULAR AMINOPEPTIDASE.
                      RNA-DIRECTED RNA POLYMERASE
                                                        HELICASE (NS3).
          POTENTIAL.
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                                                                                                                                      PROTEIN
                                                                                                                                                                                                                                                    NUCLEOCAPSID IS A COMPLEX OF
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                                 PROTEIN NS4A.
PROTEIN NS4B.
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                                                                                                                                                                                                                                                                                                                                             SHEETS R.L.,
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                                                                                                                                                                                  TRANSMEMBRANE;
                                                                                                                                                                                             CORE PROTEIN
                                                                                                                                                            a
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                      (NS5).
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Best Local :
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                                                                                                                                                                                 EMBL; X15002,
PIR; S07757; GNWYYP.
POLYPROTEIN; GLYCOPROTEIN; R
COAT PROTEIN; ENVELOPE PROTE
CONSTRUCTURAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLG_YEFV2 STANDARD; PRT; 3411 AA.

P19901;
01-FEB-1991 (REL. 17, CREATED)
01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
GENOME POLYPROTEIN (CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX
PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL
PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED
RNA POLYMERASE (EC 2.7.7.48) (NS5),
YELLOW FEVER VIRUS (STRAIN PASTEUR 17D-204).

VIRIDAB; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; FLAVIVIRIDAE;
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TRANSMEM
TRANSMEM
DOMAIN
NP_BIND
SITE
DISULFID
DISULFID
DISULFID
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DISULFID
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PROPEP
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CHAIN
                                                                                                                                                                                                                                                                               DUPUY A., DESPRES P., CAHOUR A., GIRARD M., BOULOY M.;

NUCLEIC ACIDS RES. 17:3989-3989(1989).

-!- FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION. NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.
-!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS: PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF PROTEIN C AND MRNA.

PROTEIN C AND MRNA.

EMBL; X15062; THE NUCLEOCAPSID IS A COMPLEX OF PROTEIN C AND MRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE; 89282413.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FLAVIVIRUSES
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21; Conser
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TEIN; HELICASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 101; DB 1; L
Pred. No. 3.76e-01;
14; Mismatches 27;
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BY SIMILARITY.
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POTENTIAL.
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POTENTIAL.
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POTENTIAL.
POTENTIAL.
ENVELOPE GLYCOPROTEIN M.
MAJOR ENVELOPE PROTEIN E.
NONSTRUCTURAL PROTEIN NS2A.
NONSTRUCTURAL PROTEIN NS2A.
NONSTRUCTURAL PROTEIN NS2B.
                                                                                                                                                            CELLULAR AMINOPEPTIDASE
                                                                                                                                                                               REMOVED FROM CAPSID PROTEIN
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01-APR-1993 (REL 25, LAST SE
01-FEB-1995 (REL 31, LAST AN
METHANOL UTILIZATION CONTROL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P29905;
01-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1334 GLTOPFLG-LCAFLATRIFGRRSIPVNEALAAAGLVGVLAGLAFQEMEN-FLGPIAVGGL 1391
                                                                                            EMBL; M92421; G150595; -. PIR; S32871; S32871. SENSORY TRANSDUCTION; TRA
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HARMS N., REIJNDER
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                                                                         TRANSMEMBRANE;
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                                                                                                                                                                                                                      MS N. REIJNDERS W.N. ANAZAWA H., DE PALLEN C.J.,
ISPANNING R.J.M., OLIMANN L.F., STOUTHAMER A.H.;
I. MICROBIOL. 8:457-470(1993).
I. MICROBIOL. 8:457-470(1993).
FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM MOXY/MOXX
PROBABLY INVOLVED IN THE REGULATION OF THE METHANOL DEHYDROGENASE
EXPRESSION. MAY EUNCTION AS A MEMBRANE-ASSOCIATED PROTEIN KINASE
THAT PHOSPHORYLATES MOXX IN RESPONSE TO ENVIRONMENTAL SIGNALS.
                                                                                                                                                                  (PROBABLE).
SIMILARITY: TO OTHER PROKARYOTIC
                                                                                                                                                 KINASES
                                                                                                                                                                                                         SUBCELLULAR LOCATION:
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                                                                       2871; S32871.
TRANSDUCTION; TRANSFERASE; KINASE; PHOSPHORYLATION;
MBRANE; INNER MEMBRANE; METHANOL UTILIZATION.
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Similarity 32.3%;
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LAST ANNOTATION UPDATE)
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Pred. No. 3.76e-01;
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W; ADCCF22B CRC32;
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NONSTRUCTURAL PROTEIN NS4B.
RNA-DIRECTED RNA POLYMERASE
ATP (POTENTIAL).
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   CRC32;
                                                                                                                                                                    TRANSDUCTION
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O13799;
O13799;
15-JUL-1998 (REL. 3
15-JUL-1998 (REL. 3
15-JUL-1998 (REL. 3
PUTATIVE HELICASE C
SPAC17H9.02.
                                                        SUBMITTED (MAR-1992) TO EMBL; X99720; E264527; -PIR; S19381; S19381, HYPOTHETICAL PROTEIN. SEQUENCE 586 AA; 6515
                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1992
01-MAY-1992
01-NOV-1997
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                                                                                                                                                                                                                       SEQUENCE FROM N.A. FULLER L.J., KELLY
                                                                                                                                                                                                                                                                                                                SACCHAROMYCES CEREVISIAE (BAKER EUKARYOTA; FUNGI; ASCOMYCOTINA;
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EMBL, 29897; E334274; --
HYPOTHETICAL PROTEIN; HELICASE; ATP-BINDING; NUCLEAR PROTEIN
147 154 ATP (POTENTIAL).
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Similarity 22.7%;
22; Conservative
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35; Concounting
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1030 AA;
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(REL.
(REL.
                                                                                                                                                                                                                       KELLY
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. 36, LAST SEQU
. 36, LAST ANNO
E C17H9.02 IN C
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22, LAST SEQUENCE UPDATE)
35, LAST ANNOTATION UPDATE)
KD PROTEIN IN PBN1-APA1 INT
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                                                                                                                                                                                                                          Α.,
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                                                                  65152 MW;
                                                                                                                                                                                         Ö
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                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN IN PBN1-APA1 INTERGENIC REGION
   4.48;
                                                                                                                                                                                     LEWIS C., MCKEE R.A., PE
O EMBL/GENBANK/DDBJ DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE UPDATE)
ANNOTATION UPDAT
IN CHROMOSOME I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 100; DB 1;
Pred. No. 5.14e-01;
25; Mismatches 47
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Pred.
55; M
   Score
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                                                              56434E7A CRC32;
                                                                                                                                                                                                                                                                                                                   'S YEAST).
HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HEMIASCOMYCETES
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      98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99; DB 1;
No. 7.00e-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               586
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   80
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   1:
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                                                                                                                                                                                                                          PEARSON B.M.;
   Length 586;
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Best Local :
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01-NOV-1997
                                                                                                                                     PTPJ_MOUSE STANDARD; PRT; 1238 AA. 064455; 01-NOV-1997 (REL. 35, CREATED) 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE) 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) PROTEIN-TYROSINE PHOSEHATASE ETA PRECURSOR (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THONY-MEYER L., KUNZLER P.;

J. BACTERIOL. 178.6166-6172(1996).

-!- CATALYTIC ACTIVITY: CITRATE = CIS-ACONITATE + H(2)O.

-!- PATHWAY: TRICARBOXYLIC ACID CYCLE.

-!- SUBUNIT: MONOMER (BY SIMILARITY).

-!- ACONITASE HAS AN ACTIVE (4FE-4S) AND AN INACTIVE (3FE-4S) FORMS.

THE ACTIVE (4FE-4S) CLUSTER IS PART OF THE CATALYTIC SITE THAT
           SEQUENCE FROM N.A.
STRAIN-MRL-LPR/LPR;
MEDLINE; 96140699.
                                                                    MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METAL
                                                                                                               PTPRJ OR BYP.
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00450; ACONITASE_1; 1. PROSITE; PS01244; ACONITASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=110SPC4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997
01-NOV-1997
 KURAMOCHI S., MATSUDA S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RHIZOBIACEAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LYASE;
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                                                                                                                                                                                                                                                                                                 826 LPLTFEEGTSWSSLGLK 842
                                                                                                                                                                                                                                                                                                                                           769 MKYQQEQVPLVVFAGAEYGNGSSR-DWAAKGTRLLG-VRAVIC-QSFERIHRSNLVGMGV 825
                                                                                                                                                                                                                                                                      703
                                                                                                                                                                                                                              13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERCONVERTS CITRATE, CIS-ACONITASE, AND ISOCITRATE.
SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY.
L; U56817; G1666698; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12
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                                                                                                                                                                                                                                                                                                                            LRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASV 702
                                                                                                                                                                                                                                                                  LGLD-DIHRAWRTFVLR 718
                                                                                                                           BETA-LIKE TYROSINE
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llarity 22.18;
Conservative
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LAST ANNOTATION UPDATE)
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                                                                                                                            PHOSPHATASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                        MW;
 MATSUDA Y.,
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Pred. No. 9.
24; Mismatc
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                                                                                                                                                                                                                                                                                                                                                                                                                                      IRON (IRON-SULFUR CLUSTER)
(BY SIMILARITY).
24FD4901 CRC32;
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(BY SIMILARITY).
IRON (IRON-SULFUR CLUSTER)
(BY SIMILARITY).
                                                                                  VERTEBRATA;
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 SAITOH T., OHSUGI M.,
                                                                                                                                                                                                                                                                                                                                                                                               DB 1; ; 9.52e-01
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                                                                                    TETRAPODA;
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 225 QDPSLTEILLTDLKPDTQYNATIYSQAANGTEGQPRNKVFKTNSTQVSDVRA 276
                           h 4.4%;
Similarity 28.8%;
15; Conservative
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1140
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PROTEIN TYROSINE + PHOSPHATE.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: EXPRESSED IN EVERY TISSUE EXAMINED.
-!- SIMILARITY: CONTAINS 1 PROTEIN-TYROSINE PHOSPHATASE DOMAIN.
-!- SIMILARITY: CONTAINS 8 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S LETT. 378:7-14(1996).
CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS00383; TYR_PHOSPHATASE_1; 1.
PS50056; TYR_PHOSPHATASE_2; 1.
PS50055; TYR_PHOSPHATASE_PTP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEMBRANE; REPEAT; HYDROLASE
Score 97; DB 1; I
Pred. No. 1.29e+00;
18; Mismatches 17
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FIBRONECTIN TYPE-III.
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                                                                                                                   POTENTIAL.
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W; F7C61B86 CRC32;
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DAVISON M.D., RIXON F.J., DAVISON A.J.;

J. GEN. VIROL 73:2709-2713(1992).

-!- FUNCTION: MAY BE A COMPONENT OF TRIMERIC STRUCTURES LINKING ADJACENT CAPSOMERES AT THE CAPSID SURFACE.

-!- SIMILARITY: TO OTHER HERPESVIRUSES CAPSID PROTEIN VP23.

EMBL; D10879; G221739; --
EMBL; X14112; E312332; --
EMBL; X1412; E312332; --
EMBL; X1412; E312332; --
EMBL; X1412; E312332; --
EMBL; X1412; E31
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P10202;
01-MAR-1989
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01-MAR-1989 (REL. 10,
01-DEC-1992 (REL. 24,
CAPSID PROTEIN VP23.
                                                                                                                                                                                                                                                                                                                                                                                                                                 CARASSIUS AURATUS (GOLDFISH).
EUKARYOTA; METAZOA; CHORDATA;
OSTEICHTHYES; ACTINOPTERYGII;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALFC_CARAU STANDARD; PRT; 362 AA P53448; 01-OCT-1996 (REL. 34, CREATED) 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE) 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDAT FRUCTOSE-BISPHOSPHATE ALDOLASE C (EC 4.1.2.
                                            FUNCTION.
MEDLINE; 90264854.
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIXON F.J., DAVISON M.D., DAVISON A.J., J. GEN. VIROL. 71:1211-1214(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MCGEOCH D.J., DALRYMPLE M.A., DAVISON A.J., MCNAB D., PERRY L.J., SCOTT J.E., TAYLOR P.; J. GEN. VIROL. 69:1531-1574(1988).
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VIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  191
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Similarity 34.2%;
27; Conservative
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    HOMOTETRAMER (BY
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LAST SEQUENCE UPDATE)
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Pred. No. 1.74e+00;
16; Mismatches 28
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Local Similarity 25.4%;
hes 16; Conservative
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SIMILARITY: BELONGS TO CLASS I FRUCTOSE-BISPHOS
   VOK
                                                                                                                                     WRIFVLRYRAQDPPELYFY-KYDVTGAYDTI-PQDRLTEVIASIIKPQNTYCYRRYA-V 768
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TE; PS00158; ALDOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SCHIFF BASE; GLYCOLYSIS; MULTIGENE FAMILY.

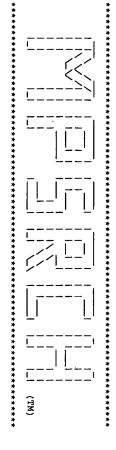
TO 0 BY SIMILARITY.

C-1-PHOSPHATE GROUP OF
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                                                                                                                                                                                                                                                                       Score 95; DB 1; Le
Pred. No. 2.35e+00;
22; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                         ESSENTIAL FOR ENHANCED ACTIVITY OF THE ENZYME TOWARD FRUCTOSE 1,6-BISPHOSPHAT AS COMPARED WITH FRUCTOSE 1-PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C-1-PHOSPHATE GROUP OF (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                          Length 362;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTIVITY OF THE 1,6-BISPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBSTRATE
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Search completed: Fri Dec 18 18:37:42 1998
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tabular output not generated. Fri Dec 18 18:39:23 1998; MasPar time 3.38 Seconds 629.739 Million cell updates/sec

Description:
Perfect Score:
Sequence: >US-08-951-733-14 (640-940) from US08951733.pep (2 of 2) 2214 940 Trom US08951733.pep (2 of 2) 1 TSRLRFIPKPDGLRPIVNMD......NLRKTVVNFPVEDEALGGTA 301

Scoring table: PAM 150 Gap 11

Searched: 77309 seqs, 7078906 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Statistics: a-issued 1:5_COMB 2:PCT9_COMB 3:backfiles1 Mean 31.637; Variance 143.394; scale 0.221

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

2 3 4 4 5 5 6 6 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result No.
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Patent No.	Sequence	Sequence	Patent No.	sequence
48, Appl	7, Appli	 Appl 	39, Appl	7, Appli	•	•	21, Appl	Appli	Appli	3, Appli		Appli	Appli	2, Appli	13, Appl	62, Appl	5	38, Appl	38, Appl	ر ا	1ddw //7
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1.35e+02	1.35e+02	1.57e+02	1.35e+02	1.57e+02	1.57e+02	1.57e+02	1.57e+02	1.57e+02	1.57e+02	1.57e+02	1.57e+02	1.57e+02	1.57e+02	1.57e+02	1.35e+02	1.35e+02	1.57e+02	1.57e+02	1.57e+02	1.57e+02	1.00e+02

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NAME: BROWDY, Roger L.	_	L-199	APPLICATION NUMBER: JP 1994/173912	PLICATION	FILING DATE: 13-JUN-1994	APPLICATION NUMBER: JP 1994/130236	PRIOR APPLICATION DATA:	FILING DATE: 05-JUN-1995	APPLICATION NUMBER: PCT/JP95/01095		CLASSIFICATION: 435			A	SOFTWARE: PatentIn Release #1.0, Version #1.30	SYSTEM: PC-DOS/MS-DOS	M PC co	TYPE: F1	H	Զ	ĸ	STATE: D.C.	CITY: Washington	STREET: 419 Seventh Street N.W., Suite 300	D NEIMARK, P.L.L.C.	ŝ	R OF SEQUENCES: 18	₹	KATO, Ikunc		APPLICANT: ASADA, Kiyozo		TAMAMOT			5	Sequence 1, Application US/08750532		Sequence 1, Application US/08750532				XXXXXX	05-08-/30-332-1 SIANDARD; FRI; 903 AA.	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

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Best Local Similarity 29.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 903 amino and Type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/08750532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-750-532-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                743 FYLRYKYDYEGLEPGLYYGRIIIDDPTTPYIEDEILNTIYIPEKFTPENNYTLTWYDI 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 5756339
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application US/08750532 Patent No. 5756339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              715 FVLRVRAQ-DP-PPELYFVKVDVTGAYDT-IPQDRL-TEVIASIIKPQNTYCVRRYAV 768
        FILING DATE: 26-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROSET L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOOMER: 25,618
                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 903 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
JENCE 903 AA; 100242 MW; 4683955 CN;
                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: MITTA, Masanori
APPLICANT: YAMAMOTO, Katsuhiko
APPLICANT: MORISHITA, Mio
APPLICANT: ASADA, Kiyozo
APPLICANT: ASADA, Kiyozo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (202) 628-5197
                                                                   PRIOR APPLICATION DATA:
                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                      PRIOR APPLICATION DATA:
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: HYPERTHERMOSTABLE PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                              APPLICATION NUMBER: PCT/JP95/01095 FILING DATE: 05-JUN-1995
                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                            COUNTRY: UZIP: 20004
                                                                                            FILING DATE: 13-JUN-1994
                                                                                                                                                                                                                                                                                                             CITY: Washington
                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                          APPLICATION NUMBER: US/08/750,532
                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                          STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                          E: BROWDY AND NEIMARK, P.L.L.C. 419 Seventh Street N.W., Suite 300
                                                                                                                                                                                                                                                                                        United States of America
                                                                                                                                                                                                                                                                                                                                                                                               TSUNASAWA, Susumu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                       JP 1994/130236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 97; DB 1;
Pred. No. 6.92e+00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15; Mismatches
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Matches
Query Match
Best Local Similarity
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                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08526964
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08526964 Patent No. 5698421 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        715 FYLRYRAQ-DP-PPELYFYKYDYTGAYDT-IPQDRL-TEVIASIIKPQNTYCYRRYAV 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              743 FYLRYKYDYEGLEPGLYYGRIIIDDPTTPYIEDEILNTIVIPEKFTPENNYTLTWYDI 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.4%;
Local Similarity 29.3%;
hes 17; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                          TELEPHONE: (216) 622-8200
TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
JENCE 1398 AA; 154545 MW; 10958156 CN;
                                                                                                                                                      REGISTRATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
                                MOLECULE TYPE:
HYPOTHETICAL:
TENCE 785 AA;
                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Golrick, Mary E
                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Guo, Huātao
APPLICANT: Yang, Jian
TITLE OF INVENTION: Nucleotide Integrase Preparation
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1398 amin
TYPE: amino acid
STRANDEDNESS: si
                                                                 TOPOLOGY:
                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                        STREET: 800 Sup
CITY: Cleveland
STATE: Ohio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                  ZIP: 44114
                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1398 amino acids
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800 Superior Avenue
                                                                                                785 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lambowitz, Alan M
                                                                 linear
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202) 737-3528
                             NO 90390 MW; 3218308
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                                                    peptide
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Pred. No. 6.92e+00;
15; Mismatches 23
Score 96; DB 1; I
Pred. No. 8.14e+00;
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                                 CN;
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          Length 785;
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Patent No.

GENERAL INFORMATION:

CORRESPONDENCE ADDRESS:

US-07-661-610C-2

STANDARD;

Matches

12;

Conservative

7;

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ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5292643man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2292-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
TELEPHONE: (703)486-2347
TELER: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/07661610C
                                                                                                                    |: |:|| || :|| :|| 644 RFIPKPDGLRPIVNMDY-VVGARTFRREKRAERLTSRVKALFSVL 687
                                                                                                                                            333 RLPPRPDRLRQRAGRAAAIVGAHRKRPPHRSERLAAHAQ-LMAAL 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Shibano, Yuji
APPLICANT: Toyoda, Hideyoshi
APPLICANT: Utsuni, Ryutaro
APPLICANT: Obata, Kazuaki
TITLE OF INVENTION: Fusaric Acid Resistant Genes
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                          MOLECULE TYPE: protein
ENCE 433 AA; 45666 MW; 736928 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FYKVDYTGAYDTIPQDRLTEVIASIIK 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: OBLON, SPIVAK, McCLELLAND, ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1755 Jefferson Davis Highway, Fourth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                            US/07/661,610C
                                                                                                                                                                                   Score 90; DB 1;
Pred. No. 2.13e+01
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                                                                 890 AA
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                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                               Sequence 5, Application US/08145006C
Patent No. 5656452
GENERAL INFORMATION:
APPLICANT: Rao, Arapplicant: Hogan,
                                                                                                                                                                                                               664 ARTERREKRAERLISRVKALFS-VLNYERARRPGLLGASVLGLDDIHRA 711
                                                                                                                                                                                                                             568 AR-YQQQSPAAALYQRSKSLSPGLLGYQQ----PSLLAAP-LGLADAHRS 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application PC/TUS9400545 GENERAL INFORMATION:
                                      Sequence 5, Application US/08145006C Patent No. 5656452
                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (617) 542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: ISM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 04:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: January 15, ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08
FILING DATE: October
APPLICATION NUMBER: 08
FILING DATE: February
APPLICATION NUMBER: 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NF-ATP, A T LYMPHOCYTE TITLE OF INVENTION: DNA-BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
TOPOLOGY: linear
NCE 890 AA; 96929 MW; 4192360 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 18-JAI
                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
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                                                                                                                                                                                                                                                                   h 3.8%;
Similarity 38.8%;
19; Conservative
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Hogan, Patrick Gerald
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jain, Jugnu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            McCaffrey, Patricia
               Rao, Anjana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rao, Anjana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     February
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                                                                                                                                                             STANDARD;
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08/017,052
08/006,067
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Pred. No. 4.65e+01
13; Mismatches 1:
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MEDIUM TYPE: Floppy

CITY: Arlington STATE: Virginia

22202

STREET:

APPLICATION NUMBER: UPPLICATE: 19910228

CLASSIFICATION: 435

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Query Match Best Local (

Match 4.18; Local Similarity 35.68;

SEQUENCE

SEQUENCE CHARACTERISTICS: LENGTH: 433 amino acid

0

i: 433 amino acids amino acid

TYPE: ami

linear

Matches

16;

Conservative

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RESULT

PCT-US94-00545-5

STANDARD;

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RESULT RESULT AC XX DEX XX DEX
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Best Local Similarity 38.8%;
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                                                                                                                                                                                                Sequence 23, Application US/08202389 Patent No. 5536636
                                                                                                                                                                                                                                                                                                                                                                                                                            664 ARTFRREKRAERLTSRVKALFS-VLNYERARRPGLLGASVLGLDDIHRA 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                       568 AR-YQQQSPAAALYQRSKSLSPGLLGYQQ---PSLLAAP-LGLADAHRS 611
                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/017,052
FILING DATE: February 11, 1993
APPLICATION NUMBER: 08/006,067
FILING DATE: January 15, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                       APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                 APPLICANT: Neel, Benjamin G.
APPLICANT: Rosenberg, Robert D.
TITLE OF INVENTION: IDENTIFICATION OF NOVEL
TITLE OF INVENTION: PHOSPHATASES HAVING SH2
                             NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 04990/007001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/145
FILING DATE: October 29, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NF-ATP, A T LYMPHOCYTE TITLE OF INVENTION: DNA-BINDING PROTEIN NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 10-
TELEFAX: 200154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
TOPOLOGY: linear
NCE 890 AA; 96929 MW; 4192360 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (617) 542-8906
                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19;
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02110-2804
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 E: Hamilton, Brook, Two Militia Drive
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                                                                                                                                         Freeman Jr., Robert M
Plutzky, Jorge
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Pred. No. 4.65e+01
13; Mismatches 1
                  Smith & Reynolds, P.
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Best Local S
Matches 1
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Sequence 2, Application PC/TUS9307213
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ATTORNEY/AGENT INFORMATION:
NAME: GRADABAN, PETLICIA
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: B199
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEPHONE: (617) 861-9340
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   729 YEVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTL 788
                                                                                                                                                                                                                                                                                              Sequence 2, Application PC/TUS9307213 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 YYV-VDPIAEYN-MPQYKLREFKVTDARDGSSRTVRQFQFIDWPEQG-VPKSGEGFIDFI 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 3.7%;
Local Similarity 22.9%;
nes 16; Conservative
                                                                                                               APPLICANT: The Government of the United States of
APPLICANT: America, as represented by The Secretary
TITLE OF INVENTION: NUCLEIC ACIDS AND AMINO ACID
TITLE OF INVENTION: SEQUENCES FOR A STRONGLY IMMUNOREACTIVE PROTEIN ENCODED
TITLE OF INVENTION: HUMAN HERPESVIRUS 6 STRAIN Z29
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein JENCE 95 AA; 11151 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 0 FILING DATE: 31-JAN-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,926
FILING DATE: 01-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
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ADDRESSEE: The Government or the Government of the ADDRESSEE: America, as represented by STREET: 6011 Executive Blvd., Suite 37 CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/0 FILING DATE: 28-FEB-1994 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid .
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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                                                                                          The Government of the United States of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
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Pred. No. 7.38e+01
23; Mismatches 2
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                                                                     The Secretary
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Best Local s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 LSKRKPDY 81
                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                              tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: protein UENCE 858 AA; 95614 MW; 3689832 CN;
                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield and Sacks, P.C
                                                                                                                                                                                                                    APPLICANT: Brenner, Michael B. APPLICANT: Parker, Christina w TITLE OF INVENTION: NO. 559411 NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/923,743
FILING DATE: 31-UULY-1992
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 496-7056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07213
FILING DATE: 19930730
          ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 858 amino acid
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 514
                                                                                                                                       COUNTRY: U
ZIP: 02210
                                                                                                                                                               STATE:
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REGISTRATION NUMBER:
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Similarity 20.6%;
14; Conservative
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                                                        us/08/199,776
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Pred. No. 8.59e+01;
22; Mismatches 29
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5594120el integrin alpha subunit
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             Query Match 3.7%;
Best Local Similarity 27.1%;
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Best Local
  Matches
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TELEFAX: 617-/20-2---
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 1178 amino acid:
TYPE: amino acid:
TYPE: amino acid:
                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application PC/TUS9502044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application PC/TUS9502044
                                                                                              TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1178 amino ac1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 3.7%;
Local Similarity 27.1%;
                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/199,776
FILING DATE: 18 February 1994
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 1178 AA; 129714 MW; 7185561 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: BOTELECOMMUNICATION INFORMATION: 617-720-3500
                                               TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 1178 AA; 129714 MW; 7185561 CN;
                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield and Sacks,
                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02044
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Novel integrin alpha subunit NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                      TYPE:
                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                              STATE: MA
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Pred. No. 8.59e+01;
14; Mismatches 18
Score 81; DB 2;
Pred. No. 8.59e+01
14; Mismatches 1
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   18;
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                          Length 1178;
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                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                 Query Match 3.7%;
Best Local Similarity 30.4%;
                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                           1224 MDGLLHYVSVISDNSGLRLLIDDQLLRNSKRLKHISSSRQSLRLGGSNFEGCISNV 1279
                                                                                                                XXXXXX
                                                                                                                                                  US-08-457-646A-4
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                                    Sequence 4, Application US/08457646A
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 24, Application PC/TUS9410261A
                                                                                                                                                                                                                        871 MENKL-FAGIRRDGLLLRL-VDDFLLVTP-HLTHAKTFLRTLVRGVPEY-GCVVNL 922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              631 RIRASTVAPGLQYFG-MSMAGGFD-ISGDGLADITVGTLGQAVVFRSR 676
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (206) 224-07: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 98101-8100
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Shelton, Dennis K.
REGISTRATION NUMBER: 26,997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Epiligrin, an Epithelial Ligand for TITLE OF INVENTION: Integrins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Carter, William G. APPLICANT: Gil, Susanna A. APPLICANT: Ryan, Maureen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RVRAQDPPPEL-YFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVR 764
                                                                                                                                                                                                                                                                                                                                                                 NECULE TYPE: protein

DESCRIPTION: E170 protein as translated from sequence of

DESCRIPTION: FIGURES 15A-15F, and as shown also in FIGURES 19A-19R

RCE 1713 AA; 189304 MW; 15276084 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/
FILING DATE: 02-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
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Application US/08457646A
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1420 Fifth Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3) 662
224-0779
NO: 24:
                                                                                                                                                  STANDARD;
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Pred. No. 8.59e+01.
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 APPLICANT:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
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Query Match 3.6%;
Best Local Similarity 25.0%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                        141 LLQAAIKYGCKVHQKTTVTEYHADKDGVAVTT 172
                                    Sequence 4, Application Patent No. 5698425 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/
FILING DATE: 01-UN-1995
APPLICATION NUMBER: 08/258
FILING DATE: 08-Jun-1994
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,646A
FILING DATE: 01-70N-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
ADDITOTION WINDED: 15 00 //57 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: CG
REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Genes for the synthesis o
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E TYPE: protein 567 AA; 65037 MW; 1552397 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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Uknes, Scott Joseph
Uknes, Scott Joseph
Genes for the synthesis of
Schupp, Thomas
Ligon, James M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     919-541-8689
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Lam, Stephen Ting
Hammer, Phillip E.
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Beck, James Joseph
Hill, Dwight Steven
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                                                                                                                                                                                                                                         STANDARD;
                                                                             US/08458076A
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                                                                                                                                                                                                                                                                                                                                                                                               Score 79; DB 1;
Pred. No. 1.16e+02
13; Mismatches 1
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IRESULT US
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Best Local S
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 567 amino acids
TYPE: amino acids
                                                                                                            Sequence 4, Application US/08258261B
                                                                                                                                                           XXXXXX
                                                                                                                                                                                US-08-258-261B-4
                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                        141 LLQAAIKYGCKVHQKTTVTEYHADKDGVAVTT 172
                                                                                                                                                                                                                           909 LVRGVPEYGCVVNLRKTVVNFPVEDEALGGTA 940
                                                                              Sequence 4; Application US/08258261B Patent No. 5639949
                                                                             Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/457,20
FILING DATE: 01-JUN-1995
APPLICATION NUMBER: 08/258,261
FILING DATE: 08-Jun-1994
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 35,129
REFERENCE/DOCKET NUMBER: CGC 150
                                                                                                                                                                                                                                                                                 Match 3.6%;
Local Similarity 25.0%;
                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/458,076A
FILING DATE: 01-UN-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein JENCE 567 AA; 65037 MW; 1552397 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Genes for the synthesis o
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 22
                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
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                                             APPLICANT:
                                                      APPLICANT:
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Uknes, Scott Joseph
VENTION: Genes for the synthesis of
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Gaffney, Thomas Deane
Lam, Stephen Ting
           Beck, James Joseph
Hill, Dwight Steven
Ryals, John Andrew
 Gaffney, Thomas Deane
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Hill, Dwight Steven
                                           Ligon, James M.
                                                     Schupp, Thomas
                                                                                                                                                                                STANDARD;
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en: CGC 1506/CIP3
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Pred. No. 1.16e+02
                                                                                                                                                                                                                                                                        13; Mismatches
                                                                                                                                                                                567
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                                                                                                                                                                                                                                                                                             Length 567;
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Best Local Similarity 25.0%;
Matches 8; Conservative
                                                                                                                                                                                       Sequence 4, Application US/08457342
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                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                        909 LVRGVPEYGCVVNLRKTVVNFPVEDEALGGTA 940
                                                                                                                                                                                                                                                                                                                    141 LLQAAIKYGCKVHQKTTVTEYHADKDGVAVTT 172 |::: || || |::: |:::: |:
                                                                                                                                                       Sequence 4, Application US/08457342 Patent No. 5662898
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 919-541-861
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           TÓPOLOGY: linear
MOLECULE TYPE: protein
UENCE 567 AA; 65037 MW; 1552397 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Rele
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 08-JUN-19
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APPLICATION NUMBER: US 08/457,205
FILING DATE: 01-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Genes for the s
TITLE OF INVENTION: antipathogenic
NUMBER OF SEQUENCES: 22
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        NUMBER OF SEQUENCES:
                    TITLE OF INVENTION:
                                                    APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Elmer, James Scott REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Ciba-Geigy Corporation STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
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Hammer, Philip Land With the Synthesis of VENTION: Genes for the synthesis of AVENTION: antipathogenic substances
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Beck, James Joseph
Hill, Dwight Steven
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Hammer, Phillip E.
Uknes, Scott Joseph
VENTION: Genes for the synthesis
                                                 Ryals, John Andrew
Gaffney, Thomas Deane
Lam, Stephen Ting
Hammer, Phillip E.
                                                                                                                                 Schupp,
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Pred. No. 1.16e+02;
13; Mismatches 11
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Search completed: Fri Dec 18 18:39:40 1998 Job time : 17 secs.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/457,342
FILING DATE: 01-JUN-1995
CLASSIFICATION NUMBER: US 08/457,205
FILING DATE: 01-JUN-1995
APPLICATION NUMBER: US 08/457,205
FILING DATE: 01-JUN-1995
APPLICATION NUMBER: 08/258,261
FILING DATE: 08-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
TELEPHONE: 919-541-8614
TELEPHONE: 919-541-8614
TELEPAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 567 amino acids
C TYPE: amino acids
TYPE: amino acids
C TYPE: protein
SEQUENCE 567 AA: 65037 MW; 1552397 CN;
                                                                                                                                                                                    Query Match 3.6%;
Best Local Similarity 25.0%;
Matches 8; Conservative
                                                                                                                   141 LLQAAIKYGCKVHQKTTVTEYHADKDGVAVTT 172 | ::: | | | | ::: | :::: |:
                                                                                             909 LVRGVPEYGCVVNLRKTVVNFPVEDEALGGTA 940
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ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Dec 18 18:23:01 1998; MasPar time 29.42 Seconds 634.618 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: >US-08-951-733-20 (1-1154) from US08951733.pep 8624

Sequence: 1 HASGQRCVLLRTWEALAPAT......TALEAAANPALPSDFKTILD 1154

Scoring table: PAM 150 Gap 11

Searched:

131922 seqs, 16180660 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 11:part12
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29

Statistics: Mean 39.946; Variance 185.025; scale 0.216

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
134 1117 1118 1118 1118 1118 1118 1118 111	Score
7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	Query Match
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21 21 21 21 21 21 21 21 21 21 21 21 21 2	DB
P91060 R23846 W40193 W40193 W404314 R854759 R5493908 R43908	ij
Predicted amino acid Fragmented human NF-H Prepro form of human Mouse OP-2 protein. Mouse OP-2 protein mop-2. Osteogenic protein mopouse osteogenic protein mo Mouse osteogenic protein mopouse osteogenic protein mopouse osteogenic protein mop-2. Mouse osteogenic protein mop-2. Murine OP-2. Murine OP-2.	Description
3.67e-01 5.36e+00 4.60e+00	Pred. No.

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37 pspsptetessagttgasaprrptgpdatpe-dstpvllrpwgrrsrrpcpsttrpltns 95

Query Match 1.6%; Best Local Similarity 29.5%; Matches 31; Conservative

Score 134; DB 1; Length 509; Pred. No. 3.67e-01; 28; Mismatches 41; Indels 5;

Gaps

5.

118 1.4 399 5 R27292 Murine osteogenic pro 118 1.4 399 10 R50239 Murine OP-2. 125 1.4 402 29 W40192 Human OP-2 protein. 125 1.4 402 26 W36855 Full length sequence 125 1.4 402 11 R60578 Osteogenic protein OP 125 1.4 402 11 R60578 Osteogenic protein No 125 1.4 402 12 R47291 Human osteogenic protein No 125 1.4 402 9 R47252 hOP2. 125 1.4 402 9 R47252 hOP2. 125 1.4 402 18 R44759 Human osteogenic prot 125 1.4 402 19 R40238 Human osteogenic prot 125 1.4 402 19 W00238 Human osteogenic prot 125 1.4 402 19 R46732 Human OP-2.PP. 126 1.4 402 10 R50732 Human OP-2. 127 1.4 402 10 R50733 Human OP-2. 128 1.4 402 10 R50733 Human OP-2. 129 1.4 402 10 R50738 Human OP-2. 120 1.4 402 10 R50738 Human OP-2. 121 1.4 402 10 R50738 Human OP-2. 125 1.4 402 10 R50738 Human OP-2. 126 1.4 402 10 R50738 Human OP-2. 127 1.4 402 10 R50738 Human OP-2. 128 1.4 402 10 R50738 Human OP-2. 129 1.4 402 10 R50738 Human OP-2. 120 1.4 402 10 R50738 Human OP-2. 121 1.4 402 10 R50738 Human OP-2. 122 1.4 402 10 R50738 Human OP-2. 123 1.4 402 10 R50738 Human OP-2. 125 1.4 402 10 R50738 Human OP-2. 126 1.4 402 10 R50738 Human OP-2. 127 1.4 402 10 R50738 Human OP-2. 128 1.4 402 10 R50738 Human OP-2. 129 1.4 402 10 R50738 Human OP-2. 120 1.4 402 10 R50738 Human OP-2. 121 1.4 402 10 R50738 Human OP-2. 122 1.4 402 10 R50738 Human OP-2. 123 1.4 402 10 R50738 Human OP-2. 125 1.4 402 10 R50738 Human OP-2. 126 1.4 402 10 R50738 Human OP-2. 127 1.4 402 10 R50738 Human OP-2. 128 1.4 402 10 R50738 Human OP-2. 129 1.4 402 10 R50738 Human OP-2. 120 1.4 402 10 R50738 Human OP-2. 121 1.4 402 10 R50738 Human OP-2. 122 1.4 402 10 R50738 Human OP-2. 125 1.4 402 10 R50738 Human OP-2. 126 1.4 402 10 R50738 Human OP-2. 127 1.4 402 10 R50738 Human OP-2. 128 1.4 402 10 R50738 Human OP-2. 129 1.4 402 10 R50738 Human OP-2. 120 1.4 402 10 R50738 Human OP-2. 121 10 10 10 10 10 10 10 10 10 10 10 10 10	45	44	43	42	41	40	39	38	37	36	35	34	33	32	32	30	29	28	27	26	25	24	23	22	21	20	19
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ALIGNMENTS

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TBRV gIII gene Fig. 3; 41pp; English. Fig. 3; 41pp; English. RMM = 54,621 dalton. It has features in common with envelope glycoproteins of other herpesviruses. The first 21 AAs are hydrophobic with the exception of Arg at position 6. This sequence could correspond to a signal peptide for membrane insertion and may well be removed during translation and transport. AAs at positions 481-498 are strongly hydrophobic and have the characteristics of a membrane-spanning region. The carboxy terminal 11 AAs have a basic charge and may function as a cytoplasmic anchor sequence. Four potential glycosylation sites are present in the region between the putative signal sequence and the transmembrane sequence. Sequence 509 AA;	24-MAY-1989: 118266. 02-NOV-1988; 118266. 03-NOV-1987; US-116197. (BAYU) Baylor College Med (NOVA-). Kit M, Kit S, Otsuka H; WPI; 89-15220/21. N-PSDB; N92357. Infectious bovine rhinotracheitis virus - which does not produce any antigenic IBRV gIII Polypeptide(s) as result of deletion and/or insertion in	P91060 standard; protein; 509 AA. P91060; P91060; P2-APR-1990 (first entry) Predicted amino acid seqence of the infectious bovine rhinotracheitis virus (IBRV) gIII polypeptide Infectious bovine rhinotracheitis virus; IBRV; gIII gene; gIII polypeptide; glycoprotein III; Bovine Herpesvirus type 1; IBRV(NG)dltkdlgIII; IBR disease vaccine; Infectious bovine rhinotracheitis disease vaccine. Infectious bovine rhinotracheitis virus (IBRV)/Bovine Herpesvirus type 1

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                                                                                                                                                                                                                                  of a sequence comprising fragments of the coding sequence of the human neurofilament subunit NF-H gene corresponding to nucleotides 1-1162 of the wild-type NF-H gene. This region contains GAGAG motifs. Frameshift mutants of the tau, ubiquitin, apolioprotein E, microtubule-associated protein 2 (MAP-2), neurofilament subunit L, M and H and amyloid A4 genes are claimed. All these genes share a common GAGAN motif (N-A, G, C or T), which is the site of common GA dinucleotide deletion(s) that cause neurodegenerative disorders. Antigenic peptides used for the production of antibodies, and small nucleic acid sequences derived from frameshift mutants are used in the diagnosis, prevention and treatment of cancer and neurodegenerative diseases, e.g. Parkinson's disease, Alzheimer's disease, Down's supranuclear palsy (PSP), amyotrophic lateral sclerosis, Huntington's disease, multiple sclerosis, and other degenerative diseases such as Garuence 386 Ab.
                                                                                                                                                Matches
                                                                                                                                                                                      Query Match
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02-OCT-1995; GB-020080.
11-JAN-1996; US-029832.
11-JAN-1996; US-029832.
(ROYA-) ROYAL NETHERLANDS ACAD AF (ROYA-) UNIV ROTTERDAM ERASMUS.
(UYUT-) UNIV STATE UTRECHT.
Burbach JPH, Grosveld FG, Van I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use of mutant genes having frame:shift mutation(s) - for developing prods. for the diagnosis, prevention and treatment of associated diseases, e.g. cancer or neuro:degenerative disease (laim 22; Fig 9; 123pp; English. w18663 and w18664 are +2 and +1 frameshift mutations, respectively, w18663 and w18664 are +2 and +1 frameshift mutations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-JUJ-1997 (first entry)
Fragmented human NF-H gene +1 frameshift mutant product.
Fragmented human NF-H gene +1 frameshift mutation; diagnosis;
Frameshift mutation product; GAGA motif; somatic mutation; diagnosis;
detection; antibody; probe; cancer; neoplasia; neurodegenerative;
Parkinson's; Alzheimer's disease; Pick's; Hantington's disease;
Down's syndrome; frontal lobe dementia; progressive supranuclear palsy;
PSP; amyotrophic lateral sclerosis; multiple sclerosis; MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 97-226235/20.
N-PSDB; T69796.
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W18664;
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FCVVSPARPAEEATSLEGALSGTRHSHPSVGRQHHAGPPSTSRPPRP
                                grgggpragalraggrggargpaeegagaaggvrlpaapppgrggra
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                                                                                                                                                               1.4%;
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Pred. No. 5.
26; Mismatc
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, T69796"
                                                                                                                                              DB 22; 15.36e+00; tches 50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New osteogenic polypeptide(s) and their dimeric proteins - useful in association with a matrix for bone reconstitution after orthopaedic and plastic surgery orthopaedic and plastic surgery bisclosure; 51-53; 69pp; English.

The sequence encodes the prepro form of human osteogenic polypeptide-2 (h0P2-PP). The protein is useful as a subunit of osteogenic and xenogenic implants in mammals. When implanted with a matrix, the polypeptide locally induces the full developmental cascade of endochondral bone formation and bone marrow differentiation. This can be used for optimal predictable bone formation to correct, eg can be used for optimal predictable bone formation to correct, and countried or congenital cranofacial and other skeletal or dental and ental and periodontal applicns., and may be used for cartilage has dental and predictable bone formation fractures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local Similarity
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W40193 standard; Prot
W40193;
08-JUN-1998 (first e
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30-APR-1992.
18-OCT-1991;
18-OCT-1990;
Mouse OP-2 protein.
Osteogenic protein; OP-2; bone morphogenic protein; OP/BMP chronic renal failure; renal therapeutic agent; disease; di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prepro form of human osteogenic polypeptide-2. Human osteogenic polypeptide-2; prepro sequence; implant; endochondral bone formation; skeletal abnormality; dental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CREA-) CREATIVE BIOMOLECULES Kuberasampath T, Oppermann H, WPI; 92-167153/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repair,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; N24522.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cleavage_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cleavage_site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-NOV-1992
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                                                                                                                                                                                                                                        253 SLP 255
                                                                                                                                                                                                                                                                                           67
                                                                                                                                                                                                                                                                                                                                                                                              12
                                                                                                                                                                                                                                                                                                                                                                        glalcalggggpglrppp-gc-pqrrlg-ardrdvg-reilavlglpgr-prprappaas 66
| :| ||:: : | || || : :|: || || || ||: :| ||: :|:
                                                                                                                                                                                                                                                                                           rlp 69
                                                                                                                                                                                                                                                                                                                                             GPPLYQLGAATQA-RPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASR 252
                                                                                                                                  standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; Protein; 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           eg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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US-599543.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label
267..3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label=
297..39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= cleavage site for signal peptide removal
257..261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= cleavage site to form mature protein
261..399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                             entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mature protein 'hOP2-A'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conserved
                                                                                                                                     399
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
Pred.
13; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treatment.
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Ozkaynak E, Rueger
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118;
No. 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seven
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
.60e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   6;
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NR N-PSDB; V10348.

PT Treatment of chronic renal failure - using an osteogenic protein/bone morphogenetic protein renal therapeutic agent or protein/bone morphogenetic protein recells

PT morphogen or renal mesenchymal progenitor cells

PT morphogen or renal mesenchymal progenitor cells

CC This sequence represents the mouse osteogenic protein, OP-2. This sequence represents the mouse osteogenic protein and having, or at risk of, chronic renal failure which comprises administering an CC osteogenic protein/bone morphogenetic protein (OP/BMP) renal therapeutic agent or morphogen. The method can be used for treating e.g. chronic cagent or morphogen. The method can be used for treating e.g. chronic constant failure, end stage renal disease, chronic diabetic nephropathy, diabetic renal hypertrophy, hypertensive constant of the protein of 
PRR 11112PRR 1112PRR 1112PRR 1112PRR 1111PRR 1112PRR 1111PRR 1112PRR 1111PRR 1112PRR 112PRR 112PRR 112PRR 112PRR 112PRR 1112PRR 1112PRR 112PRR 112PRR 112PRR 112PRR 112PRR 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         """ repartosclerosis, hypertensive glomerulosclerosis, chronic glomerulonephritis, hereditary nephritis, renal dysplasia, or a patient afflicted with e.g. glomerular hypertrophy, tubular hypertrophy, glomerulosclerosis, tubulointerstitial sclerosis or renal fibrosis. Such therapeutic agents can prevent, inhibit or delay the progressive loss of functional nephron units and the progressive decline in glomerular filtration rate (GFR) which slowly but inevitably leads to the need for renal replacement therapy.
                                                                                             03-FEB-1998
23-MAY-1995;
21-FEB-1995;
08-APR-1988;
15-AUG-1988;
15-REB-1989;
17-CCT-1989;
17-CCT-1989;
22-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-NOV-1997;
06-MAY-1997;
06-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      dimeric;
Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W44314 standard; Protein; W44314; 27-MAY-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                  US5714589-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse osteogenic protein OP2.
Mouse; osteogenic protein; subunit; endochondral bone formation; dimeric; recombinant protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cohen CM,
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06-MAY-1996; US-643321.
(CREA-) CREATIVE BIOMOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9741881-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nephropathy; glomerulopathy; hypertrophy; sclerosis; nephritis; mouse; dysplasia; fibrosis; glomerular filtration rate; GFR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        254 LP 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               n CM, Sampath | 97-558690/51.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 24; Conser
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                         447570.

US-841646.

US-179406.

US-232630.

US-315342.

US-422613.

US-422699.

US-483913.

US-569920.

US-579865.
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18..263
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1..17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KT;
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Pred. No. 4.60e+00;
12; Mismatches 22;
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PRESENTATION OF THE PROPERTY O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PT Extraction of osteogenic protein from mixture - using antibodies
pr specific for novel polypeptide chains useful as subunit(s) of
dimeric osteogenic protein(s)
pr dimeric osteogenic protein, which is
cused in the present invention. The present invention describes methods
cused in the present invention. The present invention describes methods
cused in the present invention. The present invention describes methods
cused in the present invention of the protein opposite the mixture to an antibody that
protein comprises.

CC for selectively extracting an osteogenic protein opposite the methods op
comprises a pair of oxidised subunits that are disulphide-bonded to form
a dimer, and one of the subunits has an amino acid (aa) sequence
custificiently homologous to residues 335-431 of a 431 aa protein
cc designated OPS, sequence given in the specification. In dimeric form OP
cis capable of inducing cartilage and endochondral bone formation in a
methods are used for recovering the recombinant proteins from cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-OCT-1990; US-600024
21-NOV-1990; US-621849
04-DEC-1990; US-621948
22-FEB-1991; US-660162
20-DEC-1991; US-810560
28-JAN-1992; US-82702
01-NOV-1993; US-447570
(STYC) STRYKER CORP.
US5468845-A.
21-NOV-1995.
08-APR-1988;
08-APR-1988;
15-AUG-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R85759
R85759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; osteogenic protein; hOP-1; murine; mOP-1; TGF-beta superfamily; transforming growth factor-beta; dimer; antibody; epitope; hippocampus; purification; implantable osteogenic device; bone formation; cranofacial; anomaly; skeletal; dental; endochrondral bone formation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JUN-1996 (first entry) mOP-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 98-158353/14.
N-PSDB; V15217.
                                                                                                                                                           peptide
                                                                                                                                                                                                                                                                                               protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                  peptide
                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                               non-union fracture; cartilage repair; osteoarthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 194 GPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRS 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; Protein; 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .. 1.4%;
Similarity 38.7%;
24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69
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US-660162.
US-810560.
US-827052.
US-147023.
  179406.
US-179406.
US-232630.
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US-621849.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ŗ,
                                                                                                                                                             /note= "mOP-2
17..260
                                                                                                                                                                                                                                              claim
                                                                                                                                                                                                                                                                                               /note= "Prepro-peptide"
261..399
                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                       /note-
                                                                                                                                    note-
                                                                                                                                                                                                                                              ហ្វ
                                                                                                                                    "mOP-2 peptide,
                                                                                                                                                                                                                                                                       "Mature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 118; DB 29;
Pred. No. 4.60e+00;
12; Mismatches 22;
                                                                                                                                                                                      peptide,
                                                                                                                                                                                                                                                                    mOP-2, also designated
                                                                                                                                                                                         claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 399;
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                                                                                                                                                                                                                                                                            mOP2-Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4;
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RESULT ID RESULT ID RESULT ID RESULT IT RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibodies with osteogenic protein binding specificity - used in purification of osteogenic proteins, and as antigenic proteins Disclosure; Column 139-42; 129pp; English.

PS Disclosure; Column 139-42; 129pp; English.

CC This sequence represents the murine osteogenic protein, mop-2. mop-2 the mop-2 protein can be used in the TGF-beta superfamily. Fragments CC of thee mop-2 proteins in the TGF-beta superfamily. Fragments CC of the mop-2 protein of antibodies with the penduction of antibodies with the penduction of antibodies are CC capable of binding specificities for osteogenic proteins. The antibodies are CC capable of binding specifically to an epitope of the osteogenic protein cand may be used in an implantable osteogenic device which allows predictable bone formation to correct acquired and congenital cranofactal and other skeletal or dental anomalies. They may be used to induce local endochrondral bone formation in non-union fractures and in other clinical applications including dental and periodontal applications where bone formation is required. Other potential applications include cartilage repair, e.g. in the treatment of osteograrthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 24; Conser
                                                                                                                                                                                                               W09410203-A.
11-MAY-1994.
02-NOV-1993; U10520.
03-NOV-1992; US-971091.
04-MAR-1993; US-029335.
31-MAR-1993; US-040510.
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07-SEP-1990;

18-CCT-1990;

18-CCT-1990;

21-NCV-1990;

04-DEC-1990;

04-DEC-1990;

04-DEC-1991;

22-EB-1991;

20-DEC-1991;

20-DEC-1991;

21-FEB-1992;

21-FEB-1992;

21-FEB-1993;

(STYC) STRYK
                                                                                                       Cohen CM, Kuberasampath Pang RHL, Rueger DC; WPI; 94-167392/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        R54938 standard; Protein; 3
R54938;
15-OCT-1994 (first entry)
Osteogenic protein mOP2-PP
A morphogenically active protein MOP-3 - morphogenesis in mammals Disclosure; Page 134-136; 164pp; English
                                                                                                                                                                                                                                                                                                                                                                                                           Morphogenic protein; mOP-2-PP; OP-2; mOP-2; mOP-2; tissue morphogenesis; osteogenic protein.
                                                                                    P-PSDB; Q65394
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                                                                                                                                                                                              (CREA-) CREATIVE BIOMOLECULES INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-42699

US-422699

US-422613

US-483913

US-68920

US-599543

US-616374

US-61849

US-660162

US-660162

US-821988

US-660162

US-810560

US-810560

US-810560

US-811646

US-841646
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llarity 38.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oppermann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 399
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Pred.
12; M
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                                                                                                                                                                  Oppermann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         re 118; DB 16; L
1. No. 4.60e+00;
Mismatches 22;
                                                                                                                                                                  Η,
                                                        for inducing tissue
                                                                                                                                                                  Ozkaynak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rueger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 399;
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                                            prost-menopausal or senile osteoporosis, hyperparathyroidism etc.

PS Disclosure; Page 122-123; 162pp; English.

C The sequence is that of mouse osteogenic protein 2 (mpp-2) a
a morphogenically active protein which may be used as part of a
c method for treating a bone fracture or a disease which causes or
results in bone fractures or other defects in skeletal
c microstructure. Such diseases include chronic renal failure and
c other kidney diseases, osteomalacia, vitamin D deficiency induced
osteopenia or osteoporosis, postmenopausal or senile osteoporosis,
hyperparathyroidism and Paget's disease. The methods can be used for
postmenopausal females, aged individuals and individuals undergoing
dialysis. The loss of bone mass may result from an imbalance in bone
resorption or bone formation, an imbalance of calcium or phosphate
metabolium or phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 2
                                                                                                                                                                                                                                                                                                                                                                          01-APR-1993
28-AUG-1992; U07432.
30-AUG-1991; US-752764.
30-AUG-1991; US-752857.
30-AUG-1991; US-752861.
31-JUL-1992; US-923780.
(CREA-) CREATIVE BIOMOLECULES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse osteogenic protein 2 (mOP-2).

Bone; loss; increase; fracture; post-menopausal; senile;
osteoporosis; hyperparathyroidism; skeletal microstructure de
chronic renal failure; kidney disease; osteomalacia, vitamin
deficiency-induced osteopenia, osteoporosis; Paget's disease;
bone mass; imbalance; resorption; formation; dialysis; calciu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LT 8
R33908 standard; Protein; 399
R33908;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A novel mouse morphogenic protein, OP3, has the sequence given in R54934, and is encoded by cDNA of sequence Q65390. cDNA and proteit sequences were also provided for human osteogenic protein OP1 (Q65391, R54935), mouse OP1 (Q65392, R54936), human OP2 (Q65393, R54937) and mouse OP2 (Q65394, R54938), as well as the genomic DNA sequence of human OP2 (Q65395). Generic sequences given in R54939-40 accommodate homologies between OP1, OP2, OP3 and other morphogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein family members. Sequence 399 AA;
                                                                                                                                                                                                                                                                                          WPI; 93-117208/14.
Use of morphogenic or in-vivo morphogenic-stimulating prevent bone loss or increase, used for treating bone
                                                                                                                                                                                                                                                                                                                            Pang RHL, Rueger D
WPI; 93-117208/14.
                                                                                                                                                                                                                                                                                                                                          Cohen CM, Kuberasampath T, Oppermann Pang RHL, Rueger DC, Smart JE;
                                   metabolism,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9305751-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phosphate;
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                   induced
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Similarity 38.7%;
24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       metabolism; murine.
                                     a vitamin
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genic protein 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "pro region, cleaved active protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "conserved seven cysteine skeleton"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  298..299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cocation/Qualifiers
261..399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     260
                                     D imbalance or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 118; DB 10;
Pred. No. 4.60e+00;
12; Mismatches 22;
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                                                                                                                                                                                                                                                                                                                                                              Η,
                                                                                                                                                                                                                                                                                                                                                              Ozkaynak
                                     nutritionally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  yield mature,
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                                                                                                                                                                                                                                                                                          fractures,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          defects;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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RESULT
ACCOUNT OF THE STATE OF 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PT Morphogen enriched dietary compositions and infant formula - PT capable of enhancing tissue morphogenesis, development and PT viability, e.g. in infants, aged individuals and metabolic PT disorders, e.g. anorexia nervosa, etc
PS Disclosure and Claims 25-26; Page 127-129; 160pp; English.
CC Murine osteogenic protein moP2 and proteins having at least 70% CC homology with it are preferred morphogens for inclusion in new morphogen-enriched nutritional formulations. The formulations CC are dietary compositions suitable for people at risk for tissue CC damage due to protein energy malnutrition or to altered metabolism CC function and infant formulations to enhance tissue development in CC an infant or juvenile.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 2
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Best Local
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31-JUL-1992; US-923780.
31-JUL-1992; US-922813.
16-SEP-1992; US-9246235.
04-MAR-1993; US-049335.
31-MAR-1993; US-040510.
OP-1; OP-2; CBMP2; Vgl(fx); Vgr(fx); DPP(fx); GDF-1(fx); 60A(fx); BMP3(fx); BMP5(fx); BMP5(fx); GST-0(fx); GST-0(fx); MP5(fx); MP5(fx); GST-0(fx); GST-0(fx); MP5(fx); MP5(fx); GST-0(fx); 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Muridae
                                                                                                                                                                                                                                                                    R50201 standard;
R50201;
                                                                                                                                                                                          Murine OP-2.
                                                                                                                                                                                                                             11-OCT-1994 (first entry)
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24; Conser
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larity 38.7%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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No. 4.60e+00;
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No. 4.60e+00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ozkaynak
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Best Local S
Matches 2
                                                                                                                                    Jones WK, Kuberasampa
Rueger DC, Tucker RF;
WPI; 94-065689/08.
N-PSDB; Q56201.
                                                                                                                                                                                                            17-FEB-1994.
29-JUL-1993;
31-JUL-1992;
31-MAR-1993;
31-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          effects of cancer therapy.

Claim 35-36; Page 115-117; 151pp; English.

Morphogens comprising an amino acid sequence sharing at least Morphogens comprising an amino acid sequence sharing at least 70% homology with Op-1, Op-2, CBMP2, BMP3(fx), Vg1(fx), Vgr(fx), DPP(fx), GDF-1(fx), 60A(fx) and at least 80% homology with BMP5(fx) and BMP6(fx) are useful for maintaining the integrity of the gastrointestinal tract luminal lining in a mammal, including (1) limiting epithelial cell proliferation, (2) inhibiting ulcerative lesion formation, (3) inhibiting inflammation normally associated with ulcerative diseases, and/or (4) stimulating the repair of ulcerative lesions and the regeneration of the luminal tissue.

Sequence 399 AA;
Morphogenic protein soluble complex - for regeneration of t in mammals and diagnosing tissue disorders (Claim 3; Page 75-77; 120pp; English.

This sequence represents the murine derived protein, osteogrotein, mOP-2. The mature OP-2 protein was used as at protein, mOP-2. The mature OP-2 protein of the invention. dimeric protein comprises a pair of protein subunits which associated to give a structure with morphogenic activity. subunit comprises more than 100 amino acids having a patter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-1994.
15-SEP-1993;
15-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                           R47253
R47253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maintaining integrity of gastrointestinal lining using a morphogen (stimulant) - for treating or preventing ulceration, also to inhibit endothelial cell proliferation and reduce side
                                                                                                                                                                                                                                                                                                                                 Human; hippocampus; osteogenic protein; OP-1; subunit; dimer; morphogenic activity; cysteine; morphogen; family; pro-region; complex; soluble; aqueous solvent; therapeutic composition; symptom-alleviating; co-factor; antibody; diagnosis; assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CREA-) CREATIVE BIOMOLECULES Charette MF, Cohen CM, Kuber Ozkaynak E, Pang RHL, Rueger WPI; 94-118121/14.
                                                                                                                                                                                                                                                                                                     Mus musculus.
                                                                                                                                                                                                                                                                                                                      quantitate;
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N-PSDB; Q45119.
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31-MAR-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                 CREATIVE BIOMOLECULES
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                                                                                                                                                                                 Kuberasampath
                                                                                                                                                                                                                                                                                                                      mature
                                                                                                                                                                                                             US-923780.
US-923780.
US-029335.
US-040510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.48;
llarity 38.78;
Conservative
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US-029335.
US-040510.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein;
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Pred.
12; M
                                                                                                                                                                                Oppermann
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No. 4.60e+00;
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                                                                                                                                                                                   Η,
                                                                                                                                                                                   Ozkaynak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                          osteogenic
                                                                                                                         of tissue
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Best Local
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                                                                                                                                                                                                                                                                                                         domain. OP-2 can be expressed from intact or truncated cDNA (T33444) in prokaryotic or eukaryotic host cells. Mature OP-2 and other morphogens (see also W00221-35), partic. human OP-1 (W00221), can be used to induce dentine morphogenesis, to seal dental
                                                                                                                                                                                                                                                                                                                                                                                                      Mouse embryo full-length osteogenic protein OP-2 (W00239) includes a pro-sequence and the morphogenically active mature protein sequence (see also W00224) that includes a 7-Cys C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse osteogenic protein OP-2.
Morphogen; osteogenic protein; de
morphogenesis; odontoblast; OP-2.
                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                   cavities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 61-63; 106pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tooth cavities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of morphogen(s), e.g. osteogenic proteins, on dentinalfor inducing dentine morphogenesis, desensitising teeth c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; T33444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Charette MF, Ruthe WPI; 96-412583/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-FEB-1996;
01-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09626737-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                  194 GPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRS 253
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3997
                                                                                                                                                   Similarity
24; Conse
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llarity 38.7%;
Conservative
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18..260
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                                                                                                                                                                             Score 118;
Pred. No. 4
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Pred. No. 4.60e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B
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                                                                                                                                                     Mismatches
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                                                                                                                                                                             DB 19;
.60e+00;
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                                                                                                                                                                                                                              PT Screening for compounds which modulate morphogen expression by incubating in the presence of epithelial cells which contain a PT cellular gene for morphogenic protein expression

Expression of the presence of epithelial cells which contain a PT cellular gene for morphogenic protein expression

Expression of the presents a mouse osteogenic protein-2 (mop-2). CC op-2 proteins are a group of morphogenically active proteins. Morphogens CC original when reduced, but are active as oxidised homodiners and when contained when reduced the c-terminal worphogenic proteins such as Op-2 play contained to the reduced the compound proteins such as Op-2 play contained and repair in mammals. They induce a developmental contained and repair in mammals. They induce a developmental contained of tissue-specific morphogenesis in a mammal. A novel method is described for screening a candidate compound for the ability to modulate expression of a cellular gene encoding a naturally occurring morphogenic contein. The candidate compound is incubated with epithelial cells which compressed by the cellular gene. A change in the level of the protein cellular gene. A change in the level of the protein compound to modulate expression of the candidate compound is indicative of the ability of the compound to indentify compounds which can increase or decrease morphogen considered production or levels. Such compounds can be used in the treatment of, cerdiovopathy, and cirrhosis of the liver.
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                                                                                                                                       Matches
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W36856 standard; Prótein; 399
W36856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Full length sequence of mouse osteogenic protein 2 (hOP-2).
Mouse osteogenic protein; OP; OP-2; morphogen; morphogenic protein;
embryogenesis; organ maintenance; tissue-specific morphogenesis;
                                                                                                                                                                                                       cardiomyopathy, and cirrhosis of the liver. Sequence 399 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pang RH, Rueger DC, WPI; 97-384665/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-AUG-1992; US-938021.
30-AUG-1991; US-752764.
30-AUG-1991; US-752861.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; T97882.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US5650276-A.
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   254 LP 255
                                                                    194 GPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRS 253
                                 db 89
                                                                                                12 glalcalggghgprpp-htc-pqrrlg-arerrdmqreilavlglpgr-prpraqpaaar 67
                                                                                                                                                     Local
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                                                                                                                                      Similarity 24; Conser
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M, Kuberasampath T, Oppe
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                                                                                                                                    1.4%;
larity 38.7%;
Conservative
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297..39
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mature morphogenically active
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                                                                                                                                      Pred.
12; 1
                                                                                                                                                     Score 118;
Pred. No. 4
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                                                                                                                                    DB 26; 1
1.60e+00;
ches 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ozkaynak
                                                                                                                                                                     Length 399;
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4:

R57974 standard; Protein; R57974;

399

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(first entry)

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RESULT 15
ID R33411 standard; Protein; 399 AA.
AC R33411;
DT 15-JUL-1993 (first entry)
DE Murine pro-Op-2-Pp.
KW morphogenic; osteogenic protein; developmental cascade; mOP-2;
KW mouse; inflammation; anti-inflammatory; Transforming Growth Factors
KW TGF-beta super-family; hippocampus.
OS Mus.
FH Key Location of the control of the cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IRESULT
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Matches
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W09406399-A.
31-MAR-1994.
15-SEP-1993; U08742.
15-SEP-1992; US-945285.
15-SEP-1993; US-04510.
31-MAR-1993; US-040510.
(CREA-) CREATIVE BIOMOLECULES INC.
(CREA-) CREATIVE SIMPLE COMPANY SMART SPECIAL STATES
                                                                                                                                                              W09304692-A.

18-MAR-1993.
28-AUG-1992; U07358.
30-AUG-1991; US-752764.
30-AUG-1991; US-752861.
30-AUG-1991; US-753059.
(CREA-) CREATIVE BIOMOLECULES INC.
      Cohen CM,
Pang RHL,
WPI; 93-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Morphogen-induced periodontal tissue regeneration - used in integrating as implanted tooth in tooth socket or to inhibit tissue loss associated with periodontal disease or injury Claim 28-29; Page 100-103; 132pp; English.

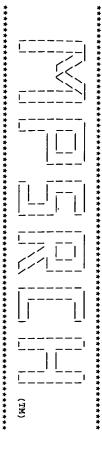
Morphogens comprising an amino acid sequence sharing at least 70% homology with OP-1, OP-2, CBMP2, Vg1(fx), Vgr(fx), DPP(fx), GDF-1(fx), 60A(fx) and at least 80% homology with BMP3(fx), BMP5(fx) and BMP6(fx) are useful for integrating an implanted tooth in a tooth socket and for inhibiting tissue loss associated with periodontal disease or injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murine OP-2; CBMP2; Vgl(fx); Vgr(fx); DPP(fx); OP-1; OP-2; CBMP2; Vgl(fx); Vgr(fx); DPP(fx); SMP5(fx); BMP5(fx); BMP5(fx); BMP5(fx); SMP5(fx); SMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mat_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; Q67314.
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Local Similarity 38.7%;
les 24; Conservative
n CM, Kuberasampath T, Oppermann RHL, Rueger DC, Smart JE; 93-100652/12.
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873..1289
/*tar-
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93..1292
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/note= "contains conserved 7 cysteine
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Pred. No. 4.60e+00;
12; Mismatches 22;
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                                                                                                                               Ozkaynak
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Claim 26; Page 126-127; 165pp; English.
Osteogenic protein (OP)-2 is a preferred morphogen for use in treating tissue damage in e.g. inflammatory disease, autoimmune disease, arthritis, psoriasis, dermatitis, diabetes an emphysema. Proteins having at least 70% homology with OP-2 amino acid sequences can also be used. See R33401 for mature mOP-2. Sequence 399 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; Q38736.
                                                                         194
 254 LP 255
                                   68 qp 69
                                                                                             12 glalcalggghgprpp-htc-pqrrlg-arerrdmqreilavlglpgr-prpraqpaaar 67
                                                                                                                                                / Match 1.4%;
Local Similarity 38.7%;
Local Similarity 38.7%;
les 24; Conservative
                                                                           GPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRS 253
                                                                                                                                                Score 118; DB 7; Le
Pred. No. 4.60e+00;
12; Mismatches 22;
                                                                                                                                                                                      Length 399
                                                                                                                                                    Indels
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Search completed: Fri Dec Job time : 125 secs. 18 18:25:06 1998

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Dec 18 18:20:51 1998; MasPar time 40.56 Seconds 971.396 Million cell updates/sec

Tabular output not generated.

>US-08-951-733-20 (1-1154) from US08951733.pep 8624

Description: Perfect Score: Sequence: 1 HASGQRCVLLRTWEALAPAT......TALEAAANPALPSDFKTILD 1154

Scoring table: PAM 150 Gap 11

Searched: 107076 segs, 34141958 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 54.111; Variance 116.481; scale 0.465

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
314 162 153 136 136 137 137 137 129 137 129 137 127 127 127 127 127 127 127 127 127 12	Score
	Query Match Length
884 5660 2240 240 310 310 310 310 310 310 310 310 310 31	•
444444444444444444444444444444444444444	BB
S53396 QQBE3 QQBE3 QCJ366 B34264 B38965 B7HUSD S16681 S01956 S11790 S11779 S10889 A28996 S27923 JQ0405 A390605 A390605 A390605 A390605 A39060533 S000533	븅
hypothetical protein BHLF1 protein - human virion protein homolo proline-rich protein salivary proline-rich homeotic protein - hu hypothetical protein - hu hypothetical protein - orf vi proline-rich protein nodulation protein nodulation protein proline-rich protein estis-specific prote gene LF3 protein - hu hypothetical 119.5K proline-rich protein testis-specific protein fordine-rich protein nodulation protein hypothetical 119.5K proline-rich protein proline-rich protein proline-rich protein hypothetical in protein proline-rich protein proline-rich protein hypothetical tumor anti nodulation protein no epithelial tumor anti	Description
1.01e-30 1.01e-30 1.87e-03 1.87e-03 1.87e-04 3.19e-04 1.87e-03 1.40e-03 1.40e-03 1.39e-02 7.89e-02 5.93e-02 5.93e-03 7.19e-03 3.71e-03 3.71e-02 7.38e-02 7.38e-02 7.38e-02 7.38e-02 7.38e-02 7.38e-02 7.38e-02	Pred. No.

BPLF1 protein -	OOBE8	_	3149	<u>.</u> ω	115	45
Ō	A35887	N	1335	μ .ω	113	44
synapsin I splice for	A35363	N	705	1.3	114	43
synapsin Ia	A30411	N	704	1.3	113	42
synapsin]	B35363	N	668	1.3	113	41
cyclin E	A56186	N	408	1.3	114	40
salivary proline-rich	PIHUB6	ب	392	1.3	115	39
hypothetical protein	S54545	N	373	1.3	114	38
HYA22 protein - human	JC5707	N	338	1.3	115	37
nodulation protein no	A28663	H	321	1.3	114	36
proline-rich	E29149	N	301	1.3	114	35
proline-rich	B48013	N	295	1.3	116	34
miaE protein	S34361	Ŋ	270	1.3	116	33
proline-rich	S22373	N	260	1.3	115	32
hypothetical protein	в36795	N	202	1.3	114	31
epithelial	S10572	N	515	1.4	119	30
extensin	S22697	N	464	1.4	124	29
chitinase	S51939	N	439	1.4	123	28
hypothetical	S09824	N	431	1.4	118	27
prpL2 protein	S52796	N	403	1.4	123	26
prepro osteogenic pro	A45056	N	402	1.4	125	25
hypothetical	S16506	N	381	1.4	125	24

ALIGNMENTS

Qy 707 DI-HRAV	Db 501 QIADRI	Qy 649 -PDGLRI	:	Qy 590 FQKNRLE	J 0 0	Qy 530 LTWKMSV	Db 330 LLKKLRI		Db 271 LSHLSRO	Query Match 3.6%; Best Local Similarity 24.3%; Matches 118; Conservative	#gene SGD #gene secreteren #map_position 12R SUMMARY #len	##experimer	##residues	##molecule_type DNA	#accession	#description	#authors		ß	DATE	ORGANISM	ALTERNATE_NAMES	ENTRY	RESULT 1
VRTEVLKV-RA-QDPPPELYEVKVDVTGAYDTIPQ-DRLTEVIASIIKPQNTYC 762	QIADRI-KEFKQRLLKKFNNVLPELYFMKFDVKSCYDSIPRMECMR-ILKDALKNENGFF 558	SNNERKLIATECKRADEGETITAENRA NA LETIVALEELEKNARETET LAISET SVO :: : : : : : : : : : : : : : : : : :		FORNITIE TRIBUTARIALIEE TYBERTH AND COMMISSIONERIONARIEE TO THE STATE OF THE STATE	re-bundanzi imbe imbabawa-i ne-mwi-Camancami chembabataba 773	: :: : : : : : : :	LLKKLRLKDFRWLFIS-DIWFTKHNFENLNQLAIC-FISWLFRQLIPKIIQTFFYCTEIS 387	: : : :: : : : :: : : :: ::: 470 LVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQE 529	SPKER-VLKFIIVILQKLLPQEMFGSKKNKGKIIKNLNLLLSLPLNGYLPFDS 329	3.6%; Score 314; DB 2; Length 884; llarity 24.3%; Pred. No. 1.01e-30; Conservative 122; Mismatches 202; Indels 44; Gaps 37;	CS SGD:EST2 ##cross-references SGD:S0004310; MIPS:YLR318w p_position 12R # #length 884 #molecular-weight 102662 #checksum 7604	##experimental_source strain S288C (AB972)	1-884 ##label DUZ	type DNA .	\$53396	of S. cerevisiae cosmid 8543.	to the gwar pata Library	\$53390	S53396	<pre>05-May-1995 #sequence_revision 01-Sep-1995 #text_change 06-Feb-1998</pre>	#formal_name Saccharomyces cerevisiae	cerevisiae) hypothetical protein L8543.12	S53396 #type complete hypothetical protein YLR318w - yeast (Saccharomyces	

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RESULT
ENTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #contents annotation; protein coding region
COMMENT The sequence contains four perfect repeats (residues 149-273,
274-398, 399-523, and 524-648).
CLASSIFICATION #superfamily human herpesvirus 4 BHLF1 protein
SUMMARY #length 660 #molecular-weight 66244 #checksum 8900
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##molecule_type DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                             Match 1.9%;
Local Similarity 30.8%;
                                                                                                                                                                                                                       QDLAAAQRC-PAGPPPTRSGA-AAQRTHR-RPPGCP 397
                                                                                                                                                                                      GALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCP
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                            v1rion #type complete
v1rion Fire homolog - bovine herpesvirus 1
alpha TIF; BHY-1 protein homolog; ICP25; Vmw65; VP16
#formal_name bovine herpesvirus 1
05-Mar-1993 #sequence_revision 05-Mar-1993 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.; Hatfull, G.; Hudson, G.S. Satchwell, S.C.; Seguin, C.; Tuffnell, P.S.; Barrell, Nature (1984) 310:207-211

DNA sequence and expression of the B95-8 Epstein-Barr v
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Sequence analysis of the 17,166 bp EcoRI Epstein-Barr virus.
09-Sep-1997
JC1306; S24229
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#formal_name human herpesvirus 4, Epstein-Barr virus
25-reb-1985 #sequence_revision 25-Feb-1985 #text_change
23-Aug-1997
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Pred. No. 6.63e-07;
34; Mismatches 60
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                                                                                                                                                                                                                                                                                                                                                                                          #authors Ann, D.K.; Carlson, D.M.
#journal J. Biol. Chem. (1985) 260:15863-15872
#title The structure and organization of a pi
for a mouse multigene family.
#cross-references MUID:86059475
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   317
                                                                                                                                                                                                                                                                                                                                        ##molecule_type DNA
##residues 1-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##cross-references EMBL:Z11610; NID:g1065725; PID:e264419; PID:
This protein interacts with cellular transcription factors
transactivate immediate early viral genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        y Match 1.8%;
Local Similarity 31.3%;
hes 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##molecule_type DNA
                                                                                                              84
                                                                                                                                                                                      24 VNGSQQGPPPPGGPQPRPPQGPPPPGGPQPRPPQGPPPPGGPQPRPPQGPPPPGGPQPRP 83
                                                                       PRRGAAPE-PERTPYGQGSWAHPG-RTRGPSDRGFCVVSPARPAEEATSLEGA-LSGTRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPPHASGPRRRIGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRRGAAPE
 SHPSVGRQHHA--GPPSTSRPPRPWDTPCPP
                     ppppGGPQPRPPQGPPPTGPQPRPTQGP-PP 172
: |: | | :: | | |: | | | : | ||
                                                                                                            PQGPPPPGGPQQRP-PQGPPPPGGPQPRPPQGPPPPAGPQPRPPQGPPPPAGPHLRPTQG
                                                                                                                                                 LGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKR
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                                                                                                                                                                                                                         h 1.6%;
Similarity 27.2%;
41; Conservative
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Carpenter, D.E.; Misra, V.
Gene (1992) 119:259-263
Gene (1992) the bovine herpesvirus 1 homologue of
Sequences of the bovine herpesvirus 1 homologue of
simplex virus type-1 alpha-trans-inducing factor
                                                                                                                                                                                                                                                                                                   1-240 ##label ANN
#superfamily proline-rich protein
#length 240 #checksum 5152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B24264 #type fragment
proline-rich protein MP3 - mouse (fragment)
#formal_name Mus musculus #common_name house mouse
09-Sep-1987 #sequence_revision 09-Sep-1987 #text_cl
03-May-1996
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#molecular-weight 54028
                                                                                                                                                                                                                         Score 136; DB 2; Lo
Pred. No. 1.87e-03;
38; Mismatches 65;
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33; 1
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Pred. No. 1.12e-05;
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RESULT ENTRY TITLE

B38965 #type complete hypothetical protein B (insertion Enterobacter agglomerans

sequence

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CONTAINS ORGANISM
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REFERENCE
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#title Length polymorphisms in human proline-rich generated by intragenic unequal crossing (*cross-references MUID:89121440
#accession $03176
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                                                                         #cross-references MUID:85289325
#accession D25372
                                                                                                                                                                       #authors
##molecule_type mRNA
##residues 1-36,'E',38-112,'T',114-115,'P',117-121,185-271,'A'
##residues 273-310 ##label MAE
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##cross-references GB:X78052; NID:g459246; PID:g459248
# #length 276 #molecular-weight 31718 #chec
                                                                                                                                                                                                                              ##status preliminary; translation not shown
##molecule_type DNA
##residues 1-38.60-112,'T',114-115,'P',117-121,185-271,'A',273-310
##residues ##label LY3
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                                                                                                                                                                                                                                                                                                                                                                                ##molecule_type DNA
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                                                                                             J. Biol. Chem. (1985) 200:11140 11100 Differential RNA splicing and post-translational cleavages the human salivary proline-rich protein gene system:
                                                                                                                                                                                                                                                                                                          S10890
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Gene (1995) 156:37-42
IS1222: analysis and distribution of a new
in Enterobacter agglomerans 339.
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03-Nov-1995 #sequence_revision 03-Nov-1995
09-Sep-1997
                                                                                                                                                   Maeda, N.; Kim, H.S.; Azen, E.A.; Smithies, O. J. Biol. Chem. (1985) 260:11123-11130
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19-Feb-1984 #sequence_revision 12-Apr-1996 #text_change
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)3176; S03175; S10890; D25372; E38355; A03295; A61294;
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Matches 4
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#accession E38355
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p_position 12p13.2-12p13.2
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##residues 241-254,'KN',257-310 ##label KAU
    259
                                       221 HPGKPEGPPPQEGNKSRSARSPPGKPQGPPQQEGNKPQGPPPPGKPQGPPPPGGNPQQPQ 280
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Local Similarity 28.2%;
es 40; Conservative
                                                                                                   QGGNQSQG-PPPHPGKPERPPP-QGG-NQSHRPPPPP-GKPER-PPPQGGNQSQG-P-PP
  RPRRGAAPEPERTPYGQGSWAHPGRTRGPSDR-GFCVVSPARPAE-EATSLEGALSGTRH
                                                                                QLGAATQARPPPHASGPRRIGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPK
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J. Blochem. (1983) 93:857-863
Amino acid sequences of glycopeptides obtained from basic proline-rich glycoprotein of human parotid saliva.
A61294
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Basic proline-rich proteins from human parotid relationships of the covalent structures of from a single individual.
                                                                                                                                                                                                                                                                                                                                                                                                                                         the list of introns may be incomplete 
#superfamily proline-rich protein 
glycoprotein; saliva; tandem repeat
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Tannin interactions with a full-length human salivary
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J. Biochem. (1983) 93:495-502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            it is unclear from the peptide sequence whether this a product of the PRB2 (PIR:PIHUPF) or PRB4 (this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino end of peptide designated protein IB-5
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241-252 ##label CHA
                                                                                                                                                                                                                                        #binding_site carbohydrate (Asn) (covalent) #status
    predicted
th 310 #molecular-weight 31351 #checksum 3960
                                                                                                                                                                                                                                                                                                                                        #domain signal sequence #status predicted #label SIG\
#product proline-rich peptide P-D #status experimenta
#label MAT\
#babel MAT\
#binding_site_carbohydrate (Asn) (covalent) #status
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                                                                                                                                                           Score 142; DB 1;
Pred. No. 3.19e-04;
41; Mismatches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OMIM:180990
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                                                                                                                                                                                                   Length 310;
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                                                                                                                                                            ##molecule_type genomic RNA
##residues 1-628 ##label MOR
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157
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                                                                                                                               ##note
                                                                                                                                              ##cross-references EMBL:X07441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  281 PGRTRGPS 288
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GPVLTETKPRTSVRQPRSATRGPSFRPILLPKV-VH-VHDDPPHSSLRPRGSRSRQLQPT
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Similarity 30.9%;
21; Conservative
                             h 1.6%;
Similarity 25.0%;
73; Conservative
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Nucleic Acids Res. (1991) 19:3742
Nucleotide sequence of a novel divencedes a DNA binding protein.
                                                                                                                                                                                                                                                          Morch, M.D.; Boyer, J.C.; Haenni, A.L.
Nucleic Acids Res. (1988) 16:6157-6173
Overlapping open reading frames revealed by complete
nucleotide sequencing of turnip yellow mosaic virus genomic
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DNA binding;
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21-Nov-1993 #sequence_revision 10-Nov-1995
17-Oct-1997
                                                                                                                                                                                                               S01955
                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein, 69K - turnip yellow mosaic virus #formal_name turnip yellow mosaic virus, TYMV 21-Nov-1993 #sequence_revision 26-May-1995 #text_change
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#length 316
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                                                                                              #length 628 #molecular-weight 69194 #checksum
                                                                                                                                                                                                                                                                                                                                                              26-May-1995
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                                                                                                                               the authors translated the codon ACG for residue
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#molecular-weight 34713
                             Score 137; DB 2; Length 628
Pred. No. 1.40e-03;
64; Mismatches 134; Indels
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Pred. No. 1.87e-03;
20; Mismatches 24;
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#title
                                                                                        #journal Eur. J. Biochem. (1991) 202:969-974
#title Gene sequence of mouse B-type proline-rich protein MP4.
Transcriptional start point and an upstream phylogenetic footprint with ets-like and rel/NFkB-like elements.
#cross-references_MVID:92111548
                                                                             #accession
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                    ##molecule_type DNA
##residues
                                                                                                                                                                                                                                                                                                                                                                                               278 WAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVGRQHHAGPPSTSR 334
                                                                                                                                                                                                                                                                                                                                                                                                                                209 RASSGPPRRSAARS-SAASGSRPAASGPAARAPAASSARTSAGEGAARGPGAPRAGW 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##residues 1-264 ##label FRA
##cross-references GB:M30023; EMBL:M37623; NID:g332561; PID:g332566
# #length 264 #molecular-weight 25613 #checksum 1957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                273 SYLPRTSPRRGLLPNPRRHRTSTGHIPPTTTTSRPTGPPSRLQRPVH-LYQSSPHTPNFRP
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       ##residues 1-300 ##label
##cross-references GB:X58438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##molecule_type DNA
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Local Similarity 28.2%;
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ORF4 protein - Orf virus
#formal_name Orf virus
23-Aug-1991 #sequence_re
31-Oct-1997
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Sequence analysis of the inverted terminal repetition in genome of the parapoxvirus, orf virus.
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in - Orf virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 129; DB 2;
Pred. No. 1.39e-02;
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NID:g53181;
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                                                                                                                                                                                                R.; Bannister, A.J.;
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#title
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Fauthors Roberts, S.G.E.; Layfield, R.; McDonald, C.J.

*authors Nucleic Acids Res. (1991) 19:5205-5211

*title The mouse proline-rich protein MP6 promoter binds

isoprenaline-inducible parotid nuclear proteins

highly conserved NFkB/rel-like site.

*cross-references MUID:92020206

*accession S22570
                                                                                                                                                                                                                                                                                                                                                                                                                      product is secreted from the cytoplasm. #cross-references MUID:91014692 #accession S11790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #authors
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##cross-references EMBL:X61126
#FICATION #superfamily proline-rich protein
#superfamily proline-rich protein
#superfamily proline-rich protein
#superfamily proline-rich protein
                                                                                                                                                                                                                                                                                                                                                                    ##molecule_type DNA
##residues 1-302 ##label DAV
   126
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                                                                                                                                                                                                                                                                                                                                                                                                           ##status
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Local Similarity 31.4%;
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                                                                                                                                                              LMIERNLTAAARSINLSQPAMSAAVRRL-RSYFRDEL-FTMRGREFVPTP-R-AEDLAPA 72
                                  L 131
                                                                     AFRALVAQCLVCVPWDA-RPPPAAPSFRQVSCLKELVARVL-QRLCERGAKNVLAFGFAL
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Similarity 25.2%;
34; Conservative
                                                                                                                                                                                                                                                                                 *superfamily regulatory protein lysR DNA binding; transcription regulation *length 302 *molecular-weight 34274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Davis, E.O.; Johnston, A.W.B.
Mol. Microbiol. (1990) 4:921-932
Analysis of three nodD genes in Rhizobium leguminosarum
biovar phaseoli; nodDl is preceded by nolE, a gene who
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #formal_name Rhizobium leguminosarum bv. phaseoli
21-Nov-1993 #sequence_revision 13-Jan-1995 #text_
16-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nodulation protein phaseoli
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protein nodD3 - Rhizobium leguminosarum
                                                                                                                                                                                                           Score 126; DB 2;
Pred. No. 3.23e-02;
28; Mismatches 46
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pred. No. 7.89e-03;
40; Mismatches 54
                                                                                                                                                                                                                                                                                                                                                                                                           conceptual translation
                                                                                                                                                                                                               46;
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#title
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #journal
#title
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                                                                                                 16-317
                                                                                                                                                                                                                                                                                                                                                               #authors
                                                                                                                                                                                                             ##molecule_type DNA
##residues 1-317 ##label
##cross-references GB:M23236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 GPPP-QGGNQSQG-PPPHPGKPEGPPP-QGG-NQSQGPPPRP-GKPE-GPPPQGGNQSQG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preliminary; translation ##molecule_type DNA ##residing
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Similarity 30.4%;
               1.5%;
Similarity 26.4%;
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proline-rich protein - human
#formal_name Homo sapiens #common_name man
07-Oct-1994 #sequence_revision 26-May-1995
08-Sep-1997
                                                             #domain signal sequence #status predicted #label SIG\
#product proline-rich protein M14 #status predicted
#problet MAT
#label MAT
#length 317 #molecular-weight 31719 #checksum 8454
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                                                                                                                                                             #superfamily proline-rich protein
                                                                                                                                                                                                                                                                                                             Molecular evolution multigene family.
                                                                                                                                                                                                                                                                                                                                              Ann, D.K.; Smith, K.; Carlson, J. Biol. Chem. (1988) 263:1088
                                                                                                                                                                                                                                                                                                                                                                                                                 proline-rich protein M14 precursor - mouse
#formal_name Mus musculus #common_name house
30-Jun-1989 #sequence_revision 30-Jun-1989 #t
20-Mar-1998
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#length 309 #molecular-weight 30
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Pred. No. 1.39e-02;
Score 132; DB 2;
Pred. No. 5.93e-03;
38; Mismatches 64
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GB:J03891; NID:g200535;
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of the mouse proline-rich protein
Insertion of a long interspersed
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SGSQPRPPVNGSQQGPPPPGGPQPRP-PQGPPPPGGPQPRPPQGPPPPGGPQPRP-PQGP 94

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                                                                                    Query Match 1.5%; Score 132; DB 2; Length 924
Best Local Similarity 28.2%; Pred. No. 5.93e-03;
Matches 37; Conservative 33; Mismatches 52; Indels
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E.P.; Freemont, P.; Dudley, K.
#journal Development (1991) 111:561-571
#title Isolation and characterisation of a testis-expressed developmentally regulated gene from the distal inversion of the mouse t-complex.
#cross-references MUID:91372153
#accession S22933
                                                                                                                                                                                                                                                                                                  #accession
                                                                                                                                                                                                                                                                                                                                              #description
                                                                                                                                                                                                                                                                                                                                                                      #submission
206 ARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRRGAA 265
                                                                                                                                                                              ##residues 1-924 ##label PAR
##cross-references EMBL:M35547; NID:g330420; PID:g330421
# #length 924 #molecular-weight 94304 #checksum
                                                                                                                                                                                                                                ##residues
                                                                                                                                                                                                                                                  ##molecule_type DNA
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##cross-references EMBL:X52128; NID:g54852; PID:g54853
##erioss-references EMBL:X52128; NID:g54852; PID:g54853
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##residues: 1-566
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Local Similarity 35.7%;
les 30; Conservation
                                            38 AAPRAPGPEPRTRLQPATPRRSGAADPADPVGHPAA-PRAPGPEPRTRLQ-PATPRRSGA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94 VTRGAPLPPSPG-KGHLGGTPSSH 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         $27923 #type complete

gene LF3 protein - human herpesvirus 4
#formal_name human herpesvirus 4, Epstein-Barr virus
19-Mar-1997 #sequence_revision 19-Mar-1997 #text_char
08-Sep-1997
                                                                                                                                                                                                                                                                                             Parker, B.D.; Bankier, A.; Satchwell, S.; Barrell, B.; Farrell, P.J.
submitted to the EMBL Data Library, August 1990
Sequence and transcription of Raji Epstein-Barr virus DNA spanning the B95-8 deletion region.
S27923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               $22933 #type complete
testis-specific protein Bs13 - mouse
#formal_name Mus musculus #common_name house mouse
22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .0-Sep-1997
                                                                                                                                                                                                                                                                          preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 127; DB 2; Length 566; Pred. No. 2.44e-02; 19; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #text_change
                                                                                         9;
                                                                                                                                                                                8997
                                                                                       Gaps
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 323 RQHHAGPPSTS 333
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                                                  PEPERTPYGQGSWAHPGRIRGPSDRG-FCVVSPARP-AEEATSLEGALSGTRHSHP-SVG 322
                                                                  ADPA-DPVGHPA-A-P-RAPGPEPRTRLQPATPRRSGAADPADPVGHPAAPRAPGPEPRT
                         RLQPATPRRSG
                         162
                                                                             151
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Search completed: Fri Dec 18 Job time : 112 secs.

18:22:43 1998

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Dec 18 18:25:25 1998; MasPar time 30.89 Seconds 1002.720 Million cell updates/sec

Tabular output not generated.

Description:
Perfect Score:
Sequence: Title:

>US-08-951-733-20 (1-1154) from US08951733.pep 8624 1 HASGQRCVLLRTWEALAPAT.....TALEAAANPALPSDFKTILD 1154

Scoring table: PAM 150 Gap 11

Searched: 74019 segs, 26840295 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swissprot

Statistics: Mean 55.898; Variance 96.260; scale 0.581

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

110 100 100 100 100 100 100 100 100 100	Result
162 153 153 1450 1450 1470 1471 1471 1471 1471 1471 1471 147	Score
	Query Match [
500 500 500 500 500 500 500 500 500 500	Length [
. مر	DB
YHLLEBY ATIN_HSVBP PREM_HUMAN PREL_HUMAN PREM_HUMAN PREM_HUMAN PREM_MOUSE NOD3_RHILE PREM_MOUSE PREM_MOUSE PREM_HUMAN UL61_HCMVA MEH1_HUMAN UL61_HSV05 VG01_HSV05 NOD1_BRAJA MATD_NEUCR PREN_HUMAN	ID
HYPOTHETICAL BHLF1 PRO ALPHA TRANS-INDUCING P SALIVARY PROLINE-RICH SALIVARY PROLINE-RICH SALIVARY PROTEIN. SALIVARY PROTEIN. SALIVARY PROTEIN SALIVARY PROTEIN PROTEIN PROTEIN D I TESTIS-SPECIFIC PROTEIN D I TESTIS-SPECIFIC PROTEIN D I MODULATION PROTEIN D I BONE MORPHOGENETIC PRODUCATION PROTEIN U DI MESENCHYME FORK HEAD PREGULATIORY PROTEIN E2. HYPOTHETICAL GENE 1 PROTEIN CAS [2] 10 [6] A) -HYD NUDULATION PROTEIN D3. NODULATION PROTEIN D3. NODULATION PROTEIN D3. MATING TYPE PROTEIN A-SALIVARY PROLINE-RICH	Description
4.64e-07 4.56e-07 4.56e-07 8.726e-08 5.26e-08 5.26e-09 3.32e-03 3.32e-03 3.32e-03 3.32e-03 3.32e-03 3.32e-03 3.32e-03 3.32e-03 5.26e-02 3.30e-02 5.40e-01 5.40e-01 5.40e-01	Pred. No.

RESULT ID AT AC P3 DT 01

IT 2
ATIN_HSVBP STANDARD; F
p30020;
01-APR-1993 (REL. 25, CREATED)

PRT;

504 AA.

45	44	43	42	41	40	39	38	37	36	35	34	ω W	32	31	30	29	28	27	26	25	24
105	105	105	107	107	107	106	106	107	115	113	108	114	113	112	110	113	111	111	110	114	114
1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.3	1.3	1.3	1.3	1.3	ω	1.3	1.3	1.3	1.3	1.3	1.3	1.3
2774	890	863	529	494	318	285	233	174	3149	1255	706	705	704	633	628	514	509	498	408	408	408
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MAPA_RAT	ACO1_ECOLI	HIS2_NEUCR	DNB2_ADE05	MFH1_MOUSE	NODD_RHILT	YAFY_ECOLI	YFJR_ECOLI	BAR1_CHITE	TEGU_EBV	MUC1_HUMAN	SYN1_BOVIN	SYN1_HUMAN	SYN1_RAT	LA17_YEAST	V70K_TYMVC	VE2_HPV5B	VE2_HPV36	VE2_HPV08	CGE3_XENLA	CGE2_XENLA	CGE1_XENLA
MICROTUBULE-ASSOCIATED	ACONITATE HYDRATASE 1	PHOSPHORIBOSYL-AMP CYC	EARLY E2A DNA-BINDING	MESENCHYME FORK HEAD P	NODULATION PROTEIN D.	HYPOTHETICAL TRANSCRIP	HYPOTHETICAL TRANSCRIP	BALBIANI RING PROTEIN	LARGE TEGUMENT PROTEIN	MUCIN 1 PRECURSOR (POL	SYNAPSINS IA AND IB.	SYNAPSINS IA AND IB (B	SYNAPSINS IA AND IB.	PROLINE-RICH PROTEIN L	69 KD PROTEIN.	REGULATORY PROTEIN E2.	REGULATORY PROTEIN E2.	REGULATORY PROTEIN E2.	G1/S-SPECIFIC CYCLIN E	G1/S-SPECIFIC CYCLIN E	G1/S-SPECIFIC CYCLIN E
1.76e+00	1.76e+00	1.76e+00	9.79e-01	9.79e-01	9.79e-01	1.31e+00	1.31e+00	9.79e-01	8.54e-02	1.59e-01	7.28e-01	1.17e-01	1.59e-01	2.17e-01	3.99e-01	1.59e-01	2.95e-01	2.95e-01	3.99e-01	1.17e-01	1.17e-01

ALIGNMENTS

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Matches
                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 93012995.

CARPENTER D.E., MISRA V.;
GENE 119:259-263(1992).

-!- FUNCTION: RESPONSIBLE FOR TRANSCRIPTIONAL ACTIVATION OF !
EARLY PROMOTERS (ALPHA GENES) (BY SIMILARITY).

-!- SIMILARITY: TO OTHER HERPESVIRUSES ALPHA TRANS-INDUCING EMBL; 211610; E264419; -.
EMBL; 211610; E264419; -.
PIR; S24229; S24229.

PIR; S24229; S24229.

TRANSCRIPTION REGULATION; TRANS-ACTING FACTOR; DNA-BINDING.
TRANSCRIPTION REGULATION; TRANS-ACTING FACTOR; DNA-BINDING.
                                                                                                                                                                                                                                                                                                                                                         P10161; P02813;
01-MAR-1989 (REL. 10, C
01-OCT-1996 (REL. 34, I
01-OCT-1996 (REL. 34, I
SALIVARY PROLINE-RICH F
                                               NON_TER
CHAIN
SEQUENCE
                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
ALPHA TRANS-INDUCING PROTEIN (ALPHA-TIF).
BOVINE HERPESVIRUS TYPE 1 (STRAIN P8-2).
                                                                                                                                                                      SAITOH E., ISEMURA S., SANADA
J. BIOCHEM. 93:495-502(1983).
                                                                                                                                                                                              SEQUENCE OF 165-234.
MEDLINE; 83186122.
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE; 89121439.
LYONS K.M., STEIN J.H., SM
GENETICS 120:255-265(1988)
                                                                                                                                                                                                                                                                                                           HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                        PRPM_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 93012995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VIRIDAE; DS-DNA ENVELOPED
[1]
                                                                                    REPEAT;
                                                                                                                                                                                                                                                                                               EUTHERIA; PRIMATES
                                                                                                                                                                                                                                                                                                                                                (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              351 APAEAGGGWRRSGSTRTRGRAARSTTGRLQRPCCGPRRRAKC-CRATP-RQRLR--ARGE 406
           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                  x07704; E265547;
A03295; PIHUSD.
S03175; S03175.
                                                                                                  180990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QHHAGPPSTSRPPRPWDTPCPPVYAET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GPACGGPSRARGGRRRASPANP-FGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRHTS-GSGAFSQ-GRRPGRVCRLGWACKARSGPARGGPGPSPVRSGLGLSR-ARGSPGP 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRRGAAPE 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PERTPVGQGSWAHPGRTRGPSDR-GF-CVV-S-PARPAEEATSLEGALSGTRHSHPSVGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 1.8%;
Similarity 31.3%;
46; Conservative
 Similarity 29.3% 43; Conservative
                                                                                    PAROTID GLAND;
                                                165
234 /
                                                                                                                         1016
                                                 ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
          1.7%;
                                                234
23676 MW;
                                                                                                                                                                                                                                                                                                                                                      CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
PROTEIN PO (ALLELE M) (CONTAINS: PEPTIDE P-D)
                                                                                     SALIVA; MULTIGENE FAMILY
                                                                                                                                                                                    SANADA K.;
                                                                                                                                                                                                                                                SMITHIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VIRUSES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 153; DB 1;
Pred. No. 1.47e-07;
33; Mismatches 56
Score 150; DB 1;
Pred. No. 4.56e-07;
41; Mismatches 53
                                                            PEPTIDE P-D.
                                                                                                                                                                                                                                                                                                           VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                ED2D4ADC
                                                                                                                                                                                                                                                0.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HERPESVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                        234
                                                 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                        ₽
                                                                                                                                                                                                                                                                                                           TETRAPODA; MAMMALIA;
 53;
                        Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
Indels
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 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
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 10;
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RESULT
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AC P
DT 0:
DT 0:
DT 0:
DT 0:
C V
RN [
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Best Local S
Matches 4
                                                                      V70K_TYMV STAN
P10357;
01-MAR-1989 (REL. 1
01-AUG-1992 (REL. 2
01-AUG-1992 (REL. 2
69 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
CHAIN
SEQUENCE
TURNIP YELLOW MOSAIC VIRUS. VIRIDAE; SS-RNA NONENVELOPE [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRB4.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRPL_HUMAN STANDARD; PRT; 276 AA.
p10162; P02813;
01-MAR-1989 (REL. 10, CREATED)
01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) (CONTAINS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE; 89121439.
LYONS K.M., STEIN J.H., SMI'S
GENETICS 120:255-265(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 207-276.
MEDLINE; 83186122.
SAITOH E., ISEMURA S., SANADA
J. BIOCHEM. 93:495-502(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X07715; E4806; PIR; A03295; PIHUSD. PIR; S03176; S03176.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134 QGGNQSQG-PPPHPGKPERPPP-QGG-NQSHRPPPPP-GKPER-PPPQGGNQSQG-P-PP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194
                                                                                                                                                                                                                                                                                                          317
                                                                                                                                                                                                                                                                                                                                                         247
                                                                                                                                                                                                                                                                                                                                                                                                           259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPPP-QGGNQSQG-PPPHPGKPERPPP-QGG-NQSHRPPPPPP-GKPER-PPPPQGGNQSQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGTRHSHPSVGRQHHAGPPSTSRPPRP
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                                                                                                                                                                                                                                                                                                          SHPSVGRQHHAGPPSTSRPPRP
                                                                                                                                                                                                                                                                                                                                                    APPAGKPQGPPPPPQGGRPPRP 268
                                                                                                                                                                                                                                                                                                                                                                                                        RPRRGAAPEPERTPVGQGSWAHPGRTRGPSDR-GFCVVSPARPAE-EATSLEGALSGTRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                     HPGKPEGPPPQEGNKSRSARSPPGKPQGPPQQEGNKPQGPPPPGKPQGPPPPGGNPQQPQ 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPK 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POOPOAPPAGKPOGPPPPPOGGRPPRP 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P19999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAROTID GLAND; SALIVA; MULTIGENE FAMILY
                          SS-RNA NONENVELOPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              207
276 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.6%;
larity 28.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1CLG
                                                                                                                                                                                                      STANDARD;
                                                                                              10, CREATED)
23, LAST SEQUENCE UPDATE)
23, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27816 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMITHIES
                                                                                                                                                                                                                                                                                                          338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 142; DB 1; Le Pred. No. 8.72e-06; 41; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEPTIDE P-D.
4838945A CRC32;
                          VIRUSES; TYMOVIRIDAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0:
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Query Match
Best Local S
Matches 4
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Best Local
                                                                                                                                                                                                                                                  MEDLINE; 89121440.
LYONS K.M., STEIN J.H., SMITHIES O GENETICS 120:267-278(1988).
EMBL; K03207; G190508; -.
EMBL; K07882; G296670; -.
HSSP; P19999; ICLG.
MIM; 168720; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRP4_HUMAN STANDARD,
p10163; P02813;
21-JUL-1986 (REL. 01, CREATED)
13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
                                                                                       REPEAT; PAROTID C
SIGNAL 1
CHAIN 17
CHAIN 40
CONFLICT 37
CONFLICT 218
SEQUENCE 247 AJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SIMILARITY: TO 65 TO 70 KD PROTEIN EMBL; X07441; G62223; ALT_SEQ. PIR; S01955; S01955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE; 88289359.

MORCH M.D., BOYER J.C., HAENNI A.L.;

NUCLEIC ACIDS RES. 16:6557-6173(1988).

-!- FUNCTION: NOT KNOWN.
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE; 89121440.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MAEDLINE; 85289325.
MAEDA N., KIM H.-S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
les 73; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDA N., KIM H.-S., AZEN E.A., SMITHIES BIOL. CHEM. 260:11123-11130(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVLPRTSPRRGLLPNPRRHRTSTGHIPPTTTSRPTGPPSRLQRPVH-LYQSSPHTPNFRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NHAQC-PYGVLLKTHCPLRA-AVTPAAGVCAREKPQGSVAAPEEEDTDPRRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYRHRRPYPLLPNPPAALPSIAYTSSRGKIHHSLPKGALPK-EGAPPPPRRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASRSLPLPKRPRRGAAPEPERTPVG-QGSWA-HPGRTRGPSDRGFCVVSPARPAEEATSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VRRPLLAPNQFHSPRQPPPLSDDPGILGPRPLAPHSTRDPPPRPI-TPGPSN-THDLRPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SFLL-SSL-R--PSLTGARRLYETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLG-
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  Similarity
40; Conse
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larity 25.0%;
Conservative
  Conservative
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1 16
3 39
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218
218
                     1.5%;
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                                                                                                                                                                                                                               MULTIGENE FAMILY; SALIVA; GLYCOPROTEIN;
                                                                    PROTEIN N1.
GLYCOSYLATED PROTEIN A
MISSING (IN REF. 2).
D -> A (IN REF. 2).
--- 67BE90B8 CRC32;
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Score 133; DB 1;
Pred. No. 2.15e-04;
40; Mismatches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERTEBRATA; TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9E64ED49 CRC32;
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  Indels
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                                               247;
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Best Local :
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                                                                                                                                                                                                                                                                                                   NOD3_RHILP STAND
P23720;
O1-NOV-1991 (REL. 20
O1-NOV-1991 (REL. 20
O1-NOV-1995 (REL. 32
NODULATION PROTEIN I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-AUG-1987
13-AUG-1987
01-OCT-1994
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MEDLINE; 91014692.

DAVIS E.O., JOHNSTON A.W.B.;

MOL. MICROBIOL. 4:921-932(1990).

MOL. FUNCTION: NODD REGULATES THE E

WHICH ENCODE OTHER NODULATION

REGULATOR OF ITS OWN EXPRESSIO
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MEDLINE; 86059475.
ANN D.K., CARLSON D.M.;
J. BIOL. CHEM. 260:15863-15872(1985).
EMBL; M12100; G200549; -.
HSSP; P19999; 1CLG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRP3
                                                                                                                               SEQUENCE FROM STRAIN-8002;
                                                                                                                                                                                                                PLASMID SYM. PROKARYOTA; GRACILICUTES;
                                                                                                                                                                                                                                                                                   NODULATION NODD3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MUS MUSCULUS (MOUSE)
EUKARYOTA; METAZOA;
                                                                                                                                                                                                RHIZOBIACEAE
                                                                                                                                                                                                                                                             RHIZOBIUM LEGUMINOSARUM (BIOVAR PHASEOLI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROLINE-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P05143;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HPSVGRQHHAGPPSTSRPPRPWDTPCPP 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AATQARPPPHAS--GPRRRLGCE-RAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPK 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RPRRGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPAR-PAEEATSLEGALSGTRHS
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7 (REL. 05,
1 (REL. 30,
1 PROTEIN 1
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llarity 26.4%;
Conservative
                                                                                                                                                      N.A
                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                   . 20, CREATED)
. 20, LAST SEQUENCE UPI
. 32, LAST ANNOTATION U
IN D III.
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5, LAST SEQUENCE UPI
0, LAST ANNOTATION (
N MP-3 (FRAGMENT).
    EXPRESSION.
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                                                                                                                                                                                                                     SCOTOBACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 131; DB 1;
Pred. No. 4.31e-04;
38; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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  EXPRESSION OF THE NOD ABCFE GENES N PROTEINS. NODD IS ALSO A NEGATIVE ION. BINDS FLAVONOIDS AS INDUCERS.
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                                                                                                                                                                                                                       RODS
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Best Local S
Matches 3
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Best Local :
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TS13_MOUSE STANDARD: PRT; 5
001755;
01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UP
01-NOV-1997 (REL. 35, LAST ANNOTATION
TESTIS-SPECIFIC PROTEIN PBS13.
                                                                                                                                                                                                                                                                                                                                         DOMAIN
DOMAIN
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DOMAIN
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PIR; S11790; S11790
                                                                                                                                                                                                                                           REPEAT
REPEAT
                                                                                                                                                                                                                                                                                          DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAZARAKIS N.D., NELKI D., LYON M.F., FREEMONT P., DUDLEY K.; DEVELOPMENT 111:561-571(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-CBA/CA; TI
MEDLINE; 91372153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
NODULATION; TRANSCRIPTION REGULATION; DNA-BINDING;
                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- TISSUE SPECIFICITY: TESTIS.
-!- DEVELOPMENTAL STAGE: FIRSTLY EXPRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- FUNCTION: POSSIBLY PLAYS AN IMPORTANT AND FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPRESSOR; PLASMID.
DNA_BIND 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---
                                                                                                                                                                                                                                                                                                                                                                                                                                        TESTIS;
                               239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 L
                                                        34 SARGTDRVGSTVARARPPSPQGPRRGAVKTAPRGPVGHGGLRTGPTSRCPQPSARAKLPS 93 :| |: | |: : : | :| | | |: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: SOME TO YEAST L; X52128; G54853; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPERMATOCYTE STAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGI:98544; TCP11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H
                               PAPGARRRGGSASRSLPL-PKRPRRGAAPEPERTPVGQGS-WAHP-GRTRGPSDRG-FCV 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AFRALVAQCLVCVPWDA-RPPPAAPSFRQVSCLKELVARVL-QRLCERGAKNVLAFGFAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IREALQHIRLNIIPWDKFTPDQSDRHFR-VS-LCDFVTVVLFQKILERLAREAPGISFDL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLRTWEALAPATP-AMPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2933;
                                                                                                                        h 1.5%;
Similarity 35.7%;
30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 1.5%;
Similarity 31.4%;
38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        SPERMATOGENESIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         302 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42 F
34274 MW;
                                                                                                                                                                                                                        61970 MW;
                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT; COI
COILED
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                                                                                                                        Score 127; !
Pred. No. 1.!
19; Mismatc
                                                                                                                                                                                          LRR 3.
W; 7A421F03 CRC32;
                                                                                                                                                                                                                                                                                                              COILED COIL (5 HEPTADS).
COILED COIL (8 HEPTADS).
COILED COIL (2 HEPTADS).
COILED COIL (10 HEPTADS).
LEUCINE-RICH REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 126; DB 1;
Pred. No. 2.37e-03;
28; Mismatches 46
                                                                                                                                                                                                                                                                    LEUCINE-RICH
LRR 1.
LRR 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H-T-H MOTIF (BY SIMILARITY).; ED62D2FA CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      COILED COIL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             566 AA
                                                                                                                                              DB 1;
.69e-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ROLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46;
                                                                                                                             30;
                                                                                                                                                                    Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9;
                                                                                                                             <u>ن</u>
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                                                                                                                             Gaps
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P05142;
P05142;
13-AUG-1987
13-AUG-1987
01-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOD1_RHISN P55359;
         REPRESSOR;
                                                   EMBL; AE000065; G2182301; PROSITE; PS00044; HTH_LYS. NODULATION; TRANSCRIPTION
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE; 97305956.
FREIBERG C.A., FELLAY R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQ
01-NOV-1997 (REL. 35, LAST ANN
NODULATION PROTEIN D I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE; 86059475.
ANN D.K., CARLSON D.M.;
J. BIOL. CHEM. 260:15863-15872(1985)
EMBL; M12099; G200547; -.
HSSP; P19999; ICLG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EUKARYOTA;
                                                                                                                                                                                                                     PERRET X.;
NATURE 387:394-401(1997).
-!- FUNCTION: NODD REGULA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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EUKARYOTA; METAZOA; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROLINE-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                  PLASMID SYM PNGR234A.
PROKARYOTA; GRACILICU
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RHIZOBIUM SP. (STRAIN NGR234).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NODD1 OR Y4AL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                          RHIZOBIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            321 VGRQHHA--GPPSTSRP-PRPWDTPCPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          195 GGPQQQPPQGPPPPGGPQPRPPQGPPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         263 GAAPE-PE-RTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 PPPPGGPQLRPPQGPPPPAGP-QPRPPQGPPPPAGPQPRPPQGPPTTGPQPRPTQGPPPT 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                295 VSPARPAEEATSLEGALSGTRHSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 VTRGAPLPPSPG-KGHLGGTPSSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 PPQGPPPPGGPQPRPPQGPPPPGGPQPRPPQGPPPGGPQQRPPQGPPPPGGPQPRPPQG 135
                                                                                                                FUNCTION: NODD REGULATES THE EXPRESSION OF THE NOD ABCFE GENES WHICH ENCODE OTHER NODULATION PROTEINS. NODD IS ALSO A NEGATIVE REGULATOR OF ITS OWN EXPRESSION. BINDS FLAVONOIDS AS INDICERS. SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SALIVA; SIGNAL.
         MULTIGENE
23 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261 AA;
00044; HTLLYSR_FAMILY; 1.
TRANSCRIPTION REGULATION; DNA-BINDING; ACTIVATOR;
MULTIGENE FAMILY; PLASMID.
H-T-H MOTIF (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (REL. 05, CREATED)
(REL. 05, LAST SEQUENCE UPDATE)
(REL. 30, LAST ANNOTATION UPDATE)
H PROTEIN MP-2 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                GRACILICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          261
26034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.48; 27.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WW;
                                                                                                                                                                                                                                                                                            BAIROCH A., BROUGHTON W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                SCOTOBACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 125;
Pred. No. 3.
33; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANNOTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
PROLINE-RICH PROTEIN
PD830DAF CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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222

320

DB 1; .32e-03;

Length 261

Indels

9

Gaps

322

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Best Local S
Matches 2
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Matches
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                                                                                                                                                                                                                        SIGNAL; G
SIGNAL
PROPEP
CHAIN
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                   CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
BONE MORPHOGENETIC PROTEIN 8A PRECURSOR (BMP-8A) (OSTEOGENIC PROTEIN
BMP8_HUMAN
                                                                                                                                                                                                                                                                                                                                   MGB;
                                                                                                                                                                                                                                                                                                                                            EMBL; M97017; G200141;
                                                                                                                                                                                                                                                                                                                                                                                       OEZKAYNAK E., SCHNEGELSBERG P.N.J., JIN D.F., CLIFFORD G.M.,
WARREN F.D., DRIER E.A., OPPERMANN H.;
J. BIOL. CHEM. 267:25220-25227(1992).
J. BIOL. CHEM. 267:25220-25227(1992).
J. BIOL. CHEM. 267:25220-25227(1992).
J. BIOL. CHEM. 267:25220-25227(1992).
J. BIOL. CHEM. 267:2520-25227(1992).
J. BIOL. CHEM. 267:2520-25227(1992).
OSTEOINDUCTIVE FACTOR RESPONSIBLE FOR THE PHENOMENON OF CONTROL OF PLAYS A ROLE IN CALCIUM REGULATION ENTRELEMENT OF PLAYS A ROLE IN CALCIUM REGULATION AND BONE HOMOSITASIS (BY SIMILIARITY).
J. SUBUNIT: HOMODIMER, DISULFIDE-LINNED.
J. SUBUNIT: HOMODIMER, DISULFIDE-LINNED.
J. SUBUNIT: HOMODIMER, DISULFIDE-LINNED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2) (OP-2).
BMP8A OR BMP8 OR BMP-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P34821;
01-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BM8A_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-EMBRYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101
                                              254
                                                                                             194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 LRTYFRDEL-FTMNGRELVPTP-R-AEALAPAVREALLHIHLSIISWDPFNPAQSDRSFR 100
                                                                     8
                                                                                                                 12 GLALCALGGGHGPRPP-HTC-PQRRLG-ARERRDMQREILAVLGLPGR-PRPRAQPAAAR 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
             <u>1</u>3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MUSCULUS
                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                    QP 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QVSCLKELVARV-LQRLCERGAKNVLAFGFALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -II-LSDFMTLMFLERVVVRVAREAPAVSFELL 131
                                                                                                                                                                                                                                                                                                                                MGI:104515; BMP8A.
                                              Ę
                                                                                             GPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRS 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPWDA-RPPPAAPSFR 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
28; Conser
                                               255
                                                                                                                                          Similarity
24; Conse
                                                                                                                                                                                                                                                                                                           GROWTH
                                                                                                                                                                                                                                                                                                                                                                                DRASTICALLY IN 10-DAY EMBRYOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93094231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US (MOUSE).
METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                        399
                                                                                                                                                                                                                261
261
298
298
327
331
155
                                                                                                                                          1.4%;
larity 38.7%;
Conservative
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                                                                                                                                                                                        AA;
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                                                                                                                                                                                                                                                                                                          FACTOR;
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                    TGF_BETA;
                                                                                                                                                                                                                260
399
364
396
398
363
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                                                                                                                                                                                        44764 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36460
                                                                                                                                                                                                                                                                                                          CYTOKINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MW;
                                                                                                                                          Pred.
12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 121; DB 1;
Pred. No. 1.25e-02;
                                                                                                                                                                 Score
                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                      BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                           INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                            BY SIMILARITY.
                                                                                                                                                                                                                                                                         BONE MORPHOGENETIC PROTEIN 8A.
                                                                                                                                                                                                                                                                                               POTENTIAL.
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FA5238EE CRC32;
                                                                                                                                                                                        7075A1ED CRC32;
                                                                                                                                                                                                                                                                                                          BONE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No.
                                                                                                                                                     118;
No. 3.
 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  399
                                                                                                                                                                                                                                                                                                                                                                                AND VIRTUALLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126
                                                                                                                                                                                                                                                                                                          CARTILAGE; GLYCOPROTEIN.
                                                                                                                                                     DB 1;
.30e-02
 A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 322;
                                                                                                                                                                Length 399
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                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                           IN 8-DAY EMBRYOS
                                                                                                                                                                                                                                                                                                                                                                                ABSENT IN
                                                                                                                                          4;
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                                                                                                                                          Gaps
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Best Local S
Matches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A OEZKAYNÁK E., SCHNEGELSBERG P.N.J., JIN D.F., CLIFFORD G.M.,
A WARREN F.D., DRIER E.A., OPPERMANN H.;
L.J. BIOL. CHEM. 267:2520-2527(1992).
C -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION. MAY BE I
C OSTEOLNDUCTIVE FACTOR RESPONSIBLE FOR THE PHENOMENON OF
C EPITHELIAL OSTEOGENESIS. PLAYS A ROLE IN CALCIUM REGULAI
C ENIDMATE: HOMODIMER, DISULFIDE-LIMKED.
C -!- SUBUNIT: HOMODIMER, DISULFIDE-LIMKED.
C -!- SUBUNIT: HOMODIMER, DISULFIDE-LIMKED.
C -!- SUBUNIT: BELONGS TO THE TGF-BETA FAMILY.
R EMBL, M97016; G189390; -.
R PIR, A45056; A45056.
                                                                                                                                                          01-AUG-1990
01-AUG-1990
01-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
CARBOHYD
         SEQUENCE FROM N.A.

MEDLINE; 90269039.

CHEE M.S., BANKIER A.T., BECK S., BOHNI R., BROWN
HORSNELL T., HUTCHISON C.A. III, KOUZARIDES T., N
PREDDIE E., SATCHWELL S.C., TOMILINSON P., WESTON
CURR. TOP. MICROBIOL. IMMUNOL. 154:125-169(1990).
EMBL; X17403; E27260; -.

PIR; S09824; S09824.
                                                                                                                                                                                             UL61_HCMVA
P16818;
                                                                                                                                       UL61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROPEP
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
BONE MORPHOGENETIC PROTEIN 8 PRECURSOR (BMP-8)
                                                                                                                                                  HYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM; 602284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P34820;
                                                                                                               VIRIDAE;
                                                                                                                           HUMAN CYTOMEGALOVIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 93094231.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EUTHERIA; PRIMATES
                                                                                                                                                                                                                                                                                                  194
                                                                                                                                                                                                                                                       253 SLP
                                                                                                                                                                                                                                                                            68 RLP 70
                                                                                                                                                                                                                                                                                                                        12
                                                                                                                                                                                                                                                                                                   GPPLYQLGAATQA-RPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASR 252
                                                                                                                                                                                                                                                                                                                         GLALCALGGGGPGLRPPP-GC-PQRRLG-ARERRDVQREILAVLGLPGR-PRPRAPPAAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P08112; 1TFG
                                                                                                                                                                                                                                                                                                                                                Similarity 39.7%;
25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS00250; TGF_BETA;
                                                                                                                DS-DNA
                                                                                                                                                            (REL.
(REL.
                                                                                                                                                                                                                                                                                                                                                                                              402
S09824.
                                                                                                                                                  PROTEIN UL61.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FACTOR;
                                                                                                                                                                                                         STANDARD;
                                                                                                                ENVELOPED
                                                                                                                                                             15,
17,
                                                                                                                                                                                                                                                                                                                                                            1.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                    263
402
367
401
158
                                                                                                                                                                                                                                                                                                                                                                                              44764
                                                                                                                                                            CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
                                                                                                          (STRAIN AD169).
DPED VIRUSES; HERPESVIRIDAE; BETAHERPESVIRINAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOKINE;
                                                                                                                                                                                                                                                                                                                                                                                              X.
                                                                                                                                                                                                                                                                                                                                              Score 125; DB 1; Lo
Pred. No. 3.32e-03;
12; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
BONE MORPHOGENETIC I
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                               INTERCHAIN (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERTEBRATA;
                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                             8F20C81B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BONE;
                                                                                                                                                                                                            431
                                                                                                                                                              UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARTILAGE; GLYCOPROTEIN.
                                                                                                                                                                                                          ₽
                                           ES T., MARTIGNETTI J.A.,
ES T., MARTIGNETTI J.A.,
WESTON K.M., BARRELL B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                     Length 402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (OSTEOGENIC PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN 8
                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGULATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ×
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                                             B.G.;
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Search completed: Fri Dec 18 18:26:40 1998 Job time: 75 secs.
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                                                                                                                                                                           Query Match 1.4%;
Best Local Similarity 28.4%;
Matches 27; Conservative
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099958;
15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
MESENCHYME FORK HEAD PROTEIN 1 (MFH-1 PROTEIN) (TRANSCRIPTION FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE; 97312712.

MIURA N., IIDA K., KAKINUMA H., YANG X.-L., SUGIYAMA T.;

GENOMICS 41:489-492(1997).

1- FUNCTION: MIGHT BE INVOLVED IN THE FORMATION OF SPECIAL

MESENCHYMAL TISSUES (BY SIMILARITY).

1- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).

1- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).

2- SIMILARITY: CONTAINS 1 FORK-HEAD DOMAIN.

EMBL; Y08223; E303016; -.

EMBL; Y08223; E303016; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00657; FORK_HEAD_1; 1.
PROSITE; PS00658; FORK_HEAD_2; 1.
PROSITE; PS50039; FORK_HEAD_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FKHL14 OR MEH1.
HOMO SAPIENS (HUMAN).
EURARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                            TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             325
                                                                       427 NHSGDLNHL-PGHTFAAQQQTFPNVREMFNSHRLG 460
                                                                                                                                 367 SPLSALNLAAGQEGALAATGHHHQHHGHHHDQAPPPPPAPQPQPTPQPGAAAAQAASWYL 426
                                                      355 YSSGDKEQLRPSFLLSSLRPSLTGARRLVETIFLG 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       268 RGGGGKPPLGSPRA-TDGNRDPG-A-GVPARPGRRMGGSSGGRGGTPGRGPERAAPGARP 324 :::| : | | | | : | : | : | | :||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                270 RTPVG-QGSWAHPGRTRGPS-DRG 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      211 HASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSAS-RSLPLPKRPRRGAAPEPE 269
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Local Similarity 32.1%;
les 27; Conservative
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                                                                                                                   SPARPAEEATSLEGALSGTRHSHPSVGRQH-HAGPPSTSRPPRPWDTPCPPVYAETKHFL 354
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163
387
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501 AA;
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                                                                                                                                                                                                                                                                                                                                            REGULATION; DNA-BINDING; NUCLEAR PROTEIN.
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396 H
421 A
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422 P
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                                                                                                                                                                                                                                    FORK-HEAD.
POLY-ARG.
HIS-RICH.
ALA/PRO-RICH.
POLY-PRO.
POLY-ALA.
POLY-ALA.
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                                                                                                                                                                           Score 125; DB 1; Length 501; Pred. No. 3.32e-03; 28; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             232AB9D7 CRC32;
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*

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Run on: Fri Dec 18 18:27:02 1998; MasPar time 60.80 Seconds

Run on: Fri Dec 18 18:27:02 1998; MasPar time 60.80 Seconds
945.090 Million cell updates/sec
Tabular output not generated.

Title: >US-08-951-733-20
Description: (1-1154) from US08951733.pep
Perfect Score: 8624
Sequence: 1 HASGQRCVLLRTWEALAPAT......TALEAAANPALPSDFKTILD 1154
Scoring table: PAM 150
Gap 11

Searched: 165420 seqs, 49795644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptrembl6

sptremb16
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 54.168; Variance 101.474; scale 0.534

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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19 20	18	17	16	15	14	13	12	11	10	9	8	7	O	Ç	4	ω	2	Ъ	Result
129 132	131	129	136	135	140	136	141	142	143	147	314	424	439	681	678	5161	8459	8465	Score
1.5 5	1.5	1.5	1.6	1.6	1.6	1.6	1.6	1.6	1.7	1.7	3.6	4.9	5.1	7.9	7.9	59.8	98.1	98.2	Query Match I
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SALIVARY PROLINE-RICH	PROLINE RICH PROTEIN.	HOMOLOGUE OF RETROVIRA	PLENTY-OF-PROLINES-10	HYPOTHETICAL 60.2 KD	POLYKETIDE SYNTHASE (HOMEOBOX PROTEIN (FRAG	IS 1222 GENE ORF-A AND	PAROTID 'O' PROTEIN (WISKOTT-ALDRICH SYNDRO	HYPOTHETICAL PROTEIN	CHROMOSOME XII COSMID	TELOMERASE CATALYTIC	TELOMERASE SUBUNIT P12	TELOMERASE REVERSE TRA	TELOMERASE REVERSE TRA	TELOMERASE REVERSE TRA	TELOMERASE CATALYTIC S	TELOMERASE REVERSE TRA	Description
3.01e-03 P 1.14e-03	_	P ω	13	P 4	7	G 3.03e-04	D 5.65e-05	F 4.02e-05	0 2.85e-05	(7.18e-06	1.71e-35	S 2.25e-57	L.	A 3.12e-111	A 1.37e-110	-	S 0.00e+00	A 0.00e+00	Pred. No.

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488 10	382 4	297 4	295 11		106 14		657 10	14	4	4	10	ᆸ	437 2	405 2	N	14	227 11		U		N	14	539 5	
004528	000599	Q16038	Q07611	Q64306	041981	060585	022835	Q85027	043516	Q15220	Q41645	Q42421	052256	068033	Q53180	Q85028	Q62107	P91497	Q17626	Q65553	006264	Q99307	002123	Q53913
SEQUENCE OF BAC F20P5	CON1.	PRB1M PROTEIN (FRAGMEN	PROLINE-RICH PROTEOGLY	PROLINE-RICH PROTEIN.	HYPOTHETICAL 9.9 KD PR	SER/ARG-RELATED NUCLEA	SF16 ISOLOG.	VIRAL PROTEINASE.	WASP INTERACTING PROTE	PRPL-2 PROTEIN.	EXTENSIN (FRAGMENT).	CHITINASE PRECURSOR.	FLHF.	EXONUCLEASE SBCD HOMOL	MPIK3030 NODD1 GENE IN		SAL	CODED FOR BY C. ELEGAN	C04G2.8.	OL36.	HYPOTHETICAL 131.9 KD	LF3 PROTEIN.	SIMILARITY TO COLLAGEN	BETA-KETOACYL SYNTHASE
1.72e-01	2.32e-01	2.32e-01	1.72e-01	2.32e-01	2.32e-01	1.48e-02	2.76e-02	9.42e-02	1.08e-02	2.02e-02	1.48e-02	2.02e-02	9.42e-02	9.42e-02	9.42e-02	9.42e-02	1.08e-02	9.42e-02	1.27e-01	7.85e-03	2.18e-03	1.14e-03	8.18e-04	4.15e-03

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SEQUENCE;
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EMBL, AF018167; G2347129; ...
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RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF
                                                                                  PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS
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                               LCSLCYGDMENKLFAGIRRDGLLLRLYDDFLLYTPHLTHAKTFLRTLYRGYPEYGCVVNL
                                                             QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL
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                       LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL
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ONCOGENE 0:0-0(1998).
EMBL; AF051911; G3005592; -.
RNA-DIRECTED DNA POLYMERASE.
SEQUENCE 1122 AA; 127977
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01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATIC
TELOMERASE REVERSE TRANSCRIPTASE.
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
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Local Similarity 62.7%;
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07, LAST ANNOTATION UPDATE)
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O13339; CREMBLREL. 05, CREATE
O1-JAN-1998 (TREMBLREL. 05, LAST S
O1-AUG-1998 (TREMBLREL. 07, LAST A
TELOMERASE REVERSE TRANSCRIPTASE 1
TRT1.
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                                  LYNE M., RAJANDREAM M.A., BARRELL B.G., VOLCKAERT G.; SUBMITTED (MAR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS EMBL; AF015783; G2340168; -.
EMBL; AF015783; E1285360; -.
EPFAM; PF00078; I'T.
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    SEQUENCE
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NAKAMURA T.M., MORIN G.B., CHAPMAN I LINGNER J., HARLEY C.B., CECH T.R.; SCIENCE 277:955-959(1997).
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                                                                                                                                                                                                                                                                                           SEQUENCE FROM
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EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                      SEQUENCE FROM N.A.
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013338;
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LINGNER J., HARLEY C.B., CECH T.R.;
SCIENCE 27:955-959(1997).
EMBL; AF015783; G2340169; -.
PFAM; PF00078; TVC.
RNA-DIRECTED DNA POLYMERASE.
SEQUENCE 989 AA; 116456 MW; FDE74202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
TELOMERASE REVERSE TRANSCRIPTASE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=972H-;
MEDLINE; 97400623.
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Local Similarity 26.4%;
nes 129; Conservative
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                                                                                       PWQVYGFVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDC 539
                                                                                                                                            PNQVFAFLRSILVRVFPKLIWGNQRIFEIILKDLETFLKLSRYESFSLHYLMSNIKISEI 399
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                                                                                                                                                                                                 ch 7.9%; Score 681; DB 3; Length 989;
l Similarity 26.3%; Pred. No. 3.12e-111;
129; Conservative 136; Mismatches 204; Indels
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Pred. No. 1.37e-110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 5.1%; Score 439; DB 5; Le Best Local Similarity 23.0%; Pred. No. 1.97e-60; Matches 142; Conservative 168; Mismatches 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O00939 PRELIMINARY;

O00939;

O1-JUL-1997 (TREMBLREL 04, C

O1-JUL-1997 (TREMBLREL 04, I

O1-JAN-1998 (TREMBLREL 05, I

TELOMERASE SUBUNIT P123.
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EMBL; U95964; G2072336; -.
SEQUENCE 1031 AA; 12256
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HYPOTRICHS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQELTW-KMSVRDCAWLRR
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                                                                                                                  RTFRREKRAERLTSRVKALFS--VLNYERARR-PGLLGASVLGLDDIHRAWRTFVLRVRA
                                                                                                                                                                     KIVNSDRKTIKLITNIKLLNSHLMLKILKNRMFKDPFGFAVFNYDDVMKKYEEFVCK-WK
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EUPLOTIDA; EUPLOTES.
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31 AA; 122562 MW;
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O35432;
O1-CAN-1998 (TREMBLREL. 05, CREATED)
O1-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
O1-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
TELOMERASE CATALYTIC SUBUNIT (FRAGMENT).
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA
                                                                                                                                                                                                                                                                                                                                                                                                                                          Q06163;
Q06163;
                                                                                                                                                                                                                                                             01-NOV-1996 (TREMBLREL 01, CREATED)
01-NOV-1996 (TREMBLREL 01, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL 07, LAST ANNOTATION UPDATE)
CHROMOSOME XII COSMID 8543.
L8543.12.
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SUBMITTED (OCT-1997)
EMBL; AF029235; G2605
              SEQUENCE FROM N.A. STRAIN-S288C (AB972); MEDLINE; 97313267. JOHNSTON M., HILLIER
                                                                                                                                                                                               SACCHAROMYCES CEREVISIAE (BAKER'S EUKARYOTA; FUNGI; ASCOMYCOTINA; HI
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nes 51; Conser
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M., HILLIER L.,
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larity 76.1%;
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8368
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O_EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WW;
                  RILES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 424; DB 11;
Pred. No. 2.25e-57;
10; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E2A06F2B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
              ۲.,
                                                                                                                                                                                               HEMIASCOMYCETES
                                                                                                                                                                                                                            YEAST)
              ALBERMANN K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
              ANDRE
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                  ANSORGE
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Best Local Similarity 24.3%;
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BENES V., BRUCKNER M., DELIUS H., DUBOIS E., DUSTERHOFT A.,
ENTIAN K.D., FLOETH M., GOFFERM A., HEBLING U., HEUMANN K.,
HEUSS-NEITZEL D., HILBERT H., HILGER F., KLEINE K., KOTTER P.,
LOUIS E.J., MESSENGUY F., MEWES H.W., MIOSGA T., MOSTL D.,
MULLER-AUER S., NENTWICH U., OBERMAIER B., PIRAVANDI E., POHL T.M.,
MULLER-AUER S., NENTWICH U., OBERMAIER B., PIRAVANDI E., POHL T.M.,
MULLER-AUER S., NENTWICH U., OBERMAIER B., PIRAVANDI E., POHL T.M.,
MULLER-AUER S., NENTWICH B., RECHMANN S., RIEGER M., RINKE M., ROSE
SCHARFE M., SCHERENS B., SCHOLLER P., SCHWARZ S.,
UNDERWOOD A.P., URRESTARAZU L.A., VANDENBOL M., VERHASSELT P.,
VIERENDEELS F., VOET M., VOLCKAERT G., VOSK H., WAMBUTT R., WEDLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA EMBL; U20618; G662136; -. SEQUENCE 884 AA; 102662 MW; 1A94320F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-S288C (AB972);
CHERRY J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-S288C (AB972);
WATERSTON R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBMITTED (FEB-1995) TO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                271 LSHLSRQSPKER-VLKFIIVILQKLLPQEMFGSKKNKGKIIKNLNLLLSLPLNGYLPFDS
                                   718
                                                                                                                                                                                                                   763
                                                                                                                                                                                                                                                                                        707
                                                                                                                                                                                                                                                                                                      501 QIADRI-KEFKQRLLKKFNNVLPELYFMKFDVKSCYDSIPRMECMR-ILKDALKNENGFF
                                                                                                                                                                                                                                                                                                                                                                             590
   939 TAFVQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           330 LLKKLRLKDFRWLFIS-DIWFTKHNFENLNQLAIC-FISWLFRQLIPKIIQTFFYCTEIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              470 LVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQE 529
                                                                      IRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGG
                                                                                                                                                               E---M-EIF-K-T---ALWVEDKCYIREDGLFQGSSLSAPIVDLVYDDLLEFYSEFKAS
                                                                                                                                                                                                                                    VRSQY-FFNTNT-G-VLKLENV-VNASRVPKPY-ELYIDNVR-TVHLSNQDVIN---VV-
|| :| : : | | | | : |: | | : : : : | | : | : | : |
                                   IQFCAM
                                                                                                                                           VR-RYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLN
                                                                                                                                                                                                                                                                                      DI-HRAWRTFVLRV-RA-QDPPPELYFVKVDVTGAYDTIPQ-DRLTEVIASIIKPQNTYC
                                                                                                                                                                                                                                                                                                                                                                                                                                 FQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRELSEAEVRQHRE-ARPALLTSRLRFIPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STYTIVYF-RHDTWNKLITPFIVEYFKTY-LVE-NNV-CRNHNSYTLSNFNHSKMRIIPK
                                                                                                       PSQDTLILKLADDFLIISTDQQQVINIKKLAMGGFQKYNAKAN-RDKILAVSSQSDDDTV
                                                                                                                                                                                                                                                                                                                                                            -PDGLRPIVNMDY-VVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETT
                                   723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 314; DB 3; Le
; Pred. No. 1.71e-35;
122; Mismatches 202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DATA
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RESULT 9 ID Q69118 AC Q69118;

PRELIMINARY;

PRT;

296 AA.

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321 VGRQHHAGPPSTSRPPRPWDTPCPPV

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RESULT 10

ID 036027;

AC 036027;

DT 01-JUN-1998 (
DE WISKOTT-ALDRA (
GN WSP1 OR SPACA (
OS SCHIZOSACCHAR (
CEUKARYOTA; FU RN [1]

RP SEQUENCE FROM (
RC STRAIN-JS21; RA SUBMITTED (
RN [2]

RP SEQUENCE FROM (
RC STRAIN-JS21; RA SUBMITTED (
CONNOR R. CE FROM (
CONNOR R. CE STRAIN-JS21; CONNOR R. CONNOR R. CONNOR R. CONNOR R. CONNOR R. CONNOR R. STRAIN-JS2 (
RA SUBMITTED (
SEC -!- SIMILARII OR (
EMBL; AF03857 (
DR EMBL
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                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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Best Local Similarity
Matches 39; Conser
                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG 1
WSP1 OR SPAC4F10.15C.
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 87284169.
PRITZNER A.J., TSAI E.C., STROMINGER J.L.,
J. VIROL. 61:2902-2909(1987).
EMBL; M17294; G807646; -.
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
HYPOTHETICAL PROTEIN (FRAGMENT).
HUMAN HERPESVIRUS TYPE 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONNOR R., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZANKEL T.C., OW D.W.;
SUBMITTED (DEC-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-JS21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAMMAHERPESVIRINAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN HERPESVIRUS TYPE 4.
VIRIDAE; DS-DNA ENVELOPED VIRUSES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                        305
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  417
                                                                                                     359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :- SIMILARITY: TO YEAST LAS17.
MBL; AF038575; G2708709; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194
                                                     262
                                                                                                                                                        202
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                                                                                                                                                                                                                                                                                                                                                            ; Z98980; E339884; -.
IN 311 317
IN 331 343
IN 361 366
ANT 248 248
ENCE 574 AA; 59605 N
                                                                                                                                                                                AANKKRPPPPPP-PSRR---NRG-KPPIGNGSSNSSLPPPPPPPPPRSNAAG-SIPLPPQGR 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASRSLPLPKRPRRGAAPEPER-TPVGQGSWAHPGRTRGPSD 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPPPTRSGAAAQ-RTHRRPPGCPRSARNPGCPRTWRR--R-SGAQRGHPPPGAGQRPSGP 146
                                                                                                SAPPPPPPPRSAPSTGRQPPPLSSSRAVSNPP--APPPAIPGRSAPALPPLGNASRTSTPP 416
                                                                                                                                                      AATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPR 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GPPLYQLGAATQARPPPHASG-PRR-R-LGCERAWNHSVREAGVPLGLPAPGA-RRRGGS 249
VPTPP-SLPPSAPPSLPPSAPPSLPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGRPAAPGAPGTPAAPGPGGGAAVPSGATPHPERGSGPAD 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 296 AA; 31393 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TREMBLREL. 06, CREATED)
(TREMBLREL. 06, LAST SQUENCE UPDATE)
(TREMBLREL. 06, LAST ANNOTATION UPDATE)
RICH SYNDROME PROTEIN HOMOLOG 1.
                                                                                                                                                                                                                                                      1.7%;
llarity 28.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.7%;
llarity 38.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                 MW;
                                                     -GRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPS
                                                                                                                                                                                                                                                                                                                                                            POLY-PRO.
POLY-PRO.
POLY-PRO.
T -> V (IN STRAIN JS21).
W; 9E84D37C CRC32;
                                                                                                                                                                                                                                                      41;
                                                                                                                                                                                                                                                         Score 143; DB 3; Lo
Pred. No. 2.85e-05;
41; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 147; DB 14;
Pred. No. 7.18e-06;
20; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D17CEF6F
  441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRC32;
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                                                                                                                                                                                                                                                                                                            Length 574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                           Indels
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Best Local Similarity
Matches 40; Conser
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MEDLINE; 96108975.
AZEN E.A., AMBERGER E., 1
AM. J. HUM. GENET. 58:14:
EMBL; S80916; G1911492;
NON_TER 1 1
                     SEQUENCE FROM N.A. STELBL H.D.; THESIS (1995), UNIV EMBL; X78052; G4592 EMBL; X81893; E2589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              000600
000600;
01-JUL-1997
01-JUL-1997
01-JUL-1997
PARCTID 'O'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q46612;
Q46612;
Q46612;
Q1-NOV-1996 (TREMBLREL. 01, CREATED)
Q1-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
Q1-JUN-1998 (TREMBLEEL. 06, LAST ANNOTATION UPDATE)
Q1-JUN-1998 (TREMBLEEL. 06, LAST ANNOTATION UPDATE)
Q1-JUN-1998 (TREMBLEEL. 06, LAST ANNOTATION UPDATE)
Q15 1222 GENE ORT-A AND ORF-B.
                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE; 96422758.
STEIBL H.D., SIDDAVATTAM
PLASMID 34:223-228(1995).
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STEIBL H.D., SIDDAVATTAM D.;
SUBMITTED (AUG-1996) TO EMBL
                                                                                                                                                                                                                                                                                                                                                               STRAIN-KLEEBERGER, 1983;
MEDLINE; 95255664.
STEIBL H.D., LEWECKE F.M.;
GENE 156:37-42(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENTEROBACTER AGGLOMERANS. PROKARYOTA; GRACILICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENTEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SHPSVGRQHHAGPPSTSRPPRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPAGKPQGPPPPPQGGRPPRP 226
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7 (TREMBLREL. 04, LAST
7 (TREMBLREL. 04, LAST
' PROTEIN (FRAGMENT).
  276
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larity 28.2%;
Conservative
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                       ), UNIVERSITAET; G459248; -. : E258949; -.
    Ā,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S8:143-153(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23656 MW;
    31718
                                                                                                                                                                                                                                                                           EMBL/GENBANK/DDBJ
                                                                                                                                                                               D.,
    Ð,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCOTOBACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 142;
Pred. No. 4
41; Mismat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAST
                                                                   BAYREUTH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CREATED)
                                                                                                                                                                                  KLINGMUELLER
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    0B54A420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No. 4.02e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 234
    CRC32;
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                                                                                                                                                                                                                                                                           DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9;
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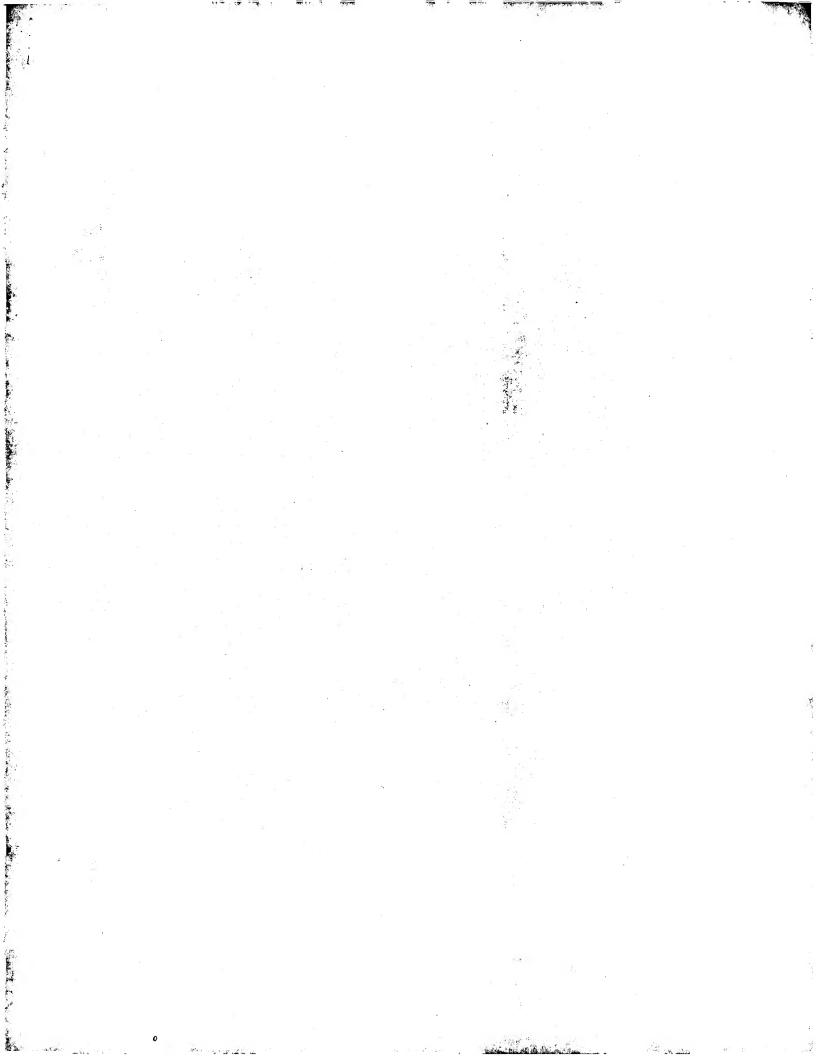
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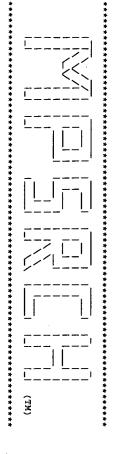
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.6%;
Best Local Similarity 30.9%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 1.6%;
Best Local Similarity 33.7%;
Matches 30; Conservative
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01-NOV-1996
01-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            054226;
01-JUN-1998 (TREMBLREL. 06, CREATOLL 06, LASTOLL 06, LASTOLL 07, LASTO
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Q99076;
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DNA-BINDING; NUCLEAR PROTEIN; HOMEOBOX;
NON_TER 1 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEGUCHI Y., KEHRL J.H.;
NUCLEIC ACIDS RES. 19:3742-3742(1991).
NUCLEIC SIMILARITY: STRONG WITH OTHER "ANTP-TYPE"
--- SIMILARITY: STRONG WITH OTHER "ANTP-TYPE"
EMBL; X56537; E30256; ALT_SEQ.
PIR; S16681; S16681.
                                                                              SALAH-BEY K., DOUMITH M., MICHEL J.M., HAY LEADLAY P.F., RAYNAL M.C.; SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ EMBL, Y14332; E1228185; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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HOMO SAPIENS (HUMAN).
HOMO SAPIENS (HUMAN).
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-NRRL2338;
                                                                                                                                                                                                                                                                                                                                                                                                    SACCHAROPOLYSPORA ERYTHRAEA (STREPTOMYCES PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; I
    SEQUENCE
                                                  NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-TONSIL;
MEDLINE; 91305125.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HOMEOBOX PROTEIN (FRAGMENT)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  644 RFIPKPDGLRPIVNMDYVVGA-RTFRREK 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RPWSTASSDCSYGRIGIAPRGPAT-SPRPSRSPAAQDRSRPARSAPGPAASPGGPGAWTH 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGRTRGPS 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RAWNHSVREAGV-PLGLPAPGARRRGGSASRSLPLPKRPRRG-AAPEPERTPVGQGSWAH 280
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112
316 AA;
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(TREMBLREL.)
    373 AA;
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121 H
34713 MW;
    40872 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06, CREATED)
06, LAST SEQUENCE UPDATE)
07, LAST ANNOTATION UPDAT
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Pred. No. 3.03e-04;
20; Mismatches 24
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Pred. No. 5.65e-05;
23; Mismatches 3(
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H-T-H MOTIF.
; 1531E766 CRC32;
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                                                                                                                                     BANKS
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041935 PRELIMINARY;
041935;
041935;
01-JAN-1998 (TREMBLREL 05, LAST
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O1-JAN-1998 (TREMBLREL 05, LAST
01-JAN-1998 (TREMBLREL 05, LAST
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Best Local S
Matches 4
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Best Local 9
                                                                                                                                                Matches
                                                                                                                                                                                                         LATREILLE P., WAMSLEY P., V
SUBMITTED (APR-1997) TO EME
EMBL; U97553; G2317934; -.
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                         MEDLINE; 97366649.
VIRGIN H.W. IV, LATREILLE P.,
DAL CANTO A.J., SPECK S.H.;
J. VIROL. 71:5894-5904(1997).
                                                                                                                                                                                                                                                                                                                                                                                 MURINE HERPESVIRUS 68. VIRUSES; DSDNA VIRUSES,
                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                            STRAIN-WUMS;
                                                                                                                                                                                                                                                                                                                                                STRAIN-WUMS;
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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 310
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                                                 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   335 PPRP 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 1.6%;
Local Similarity 32.3%;
                                                                                                                                              Match 1.6%;
Local Similarity 27.6%;
les 45; Conservative
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                                                               ARIPDLPGPLPSWGPDPRPPPRELGP-GSPT-SPAPSRAGARIPRPSRPPPELGP--G
                                                                                               PPLYQLGAATQARPPPHASGPRRR-L-GCERAWNHSVREA-GVP-LGLPAPGARRRGGSA 250
                                                                                                                      PPP-ELGPGSPTSPAPSRAGARIPDLPGPLPSWGPDPRPPRPPPELGPGSPTSPAPSRAG
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                      SPRFPRPSRPP--PELGPGSPDLPGPLPSWG-PDPPTFPAPSR
  ALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKH
                                                 SRSLPLPKR-PRRGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEG
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                                                                                                                                                                                                585 AA;
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                                                                                                                                                                                                                                                 WATERSTON R.H.;
                                                                                                                                                                                                                                                                                                                                                                                 RNA STAGE;
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LAST ANNOTATION UPDATE)
                                                                                                                                              Score 135; DB 14;
Pred. No. 4.23e-04;
37; Mismatches 68
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Pred. No. 7.93e-05;
27; Mismatches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                        WAMSLEY
                                                                                                                                                                                                B35C72E5 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                   HERPESVIRIDAE;
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                                                                                                                                                                       Length 585;
  352
                         496
                                                                                                                                                Indels 13;
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                                                                                                                                                Gaps
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MPsrch_pp protein - protein database search, using Smith-Waterman.algorithm

Run on: Fri Dec 18 18:30:31 1998; MasPar time 9.93 Seconds 823.071 Million cell updates/sec

Tabular output not generated.

Title:

Description:
Perfect Score:
Sequence: >US-08-951-733-20 (1-1154) from US08951733.pep 8624 1 HASGORCVLLRTWEALAPAT......TALEAAANPALPSDEKTILD 1154

Scoring table: PAM 150 Gap 11

Post-processing: Minimum Match 0% Listing first 45 summaries

77309 seqs, 7078906 residues

Searched:

Database: a-issued 1:5_COMB 2:PCT9_COMB 3:backfiles1

Statistics: Mean 37.265; Variance 182.038; scale 0.205

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
11188 11188 11188 11188 11188 11188 11188 11188 11188 11188	Score
	Query Match
00000000000000000000000000000000000000	Length
4484444488884884844884	BB
US-08-147- PCT-US-20- US-08-248- US-08-248- US-08-248- US-08-248- US-08-479- US-08-479- US-08-48- PCT-US-3- PCT-US-3	Ħ
Sequence 27, Sequence 27, Sequence 23, Sequence 23, Sequence 10, Sequence 10, Sequence 11, Sequence 11, Sequence 23, Sequence 12, Sequence 23, Sequence 24, Seque	Description
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2.06e+000 2.06e+000	Pred. No.

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	7.05e-01	7.05e-01	7.05e-01	7.05e-01	7.05e-01	7.05e-01	7.05e-01	/.U5e-U1													

ALIGNMENTS

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RESULT
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                                                                                                                               US-08-447-570-27
                                                 Sequence 27, Application US/08447570
                                                                                                                                                                                                                                                                                                                                              SEQUENCE
               Sequence 27, Application Patent No. 5714589
Patent No. 5714589
GENERAL INFORMATION:
                                                                                                                                                                                                                                       194 GPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRS 253
                                                                                                                                                                                   254 LP 255
                                                                                                                                                                                                                                                                                   1.48;
Local Similarity 38.78;
les 24; Conservation
                                                                                                                                                                                                             68 QP 69
                                                                                                                                                                                                                                                                12 GLALCALGGGHGPRPP-HTC-PQRRLG-ARERRDMQREILAVLGLPGR-PRPRAQPAAAR 67
                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 617/248-7100 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
JENCE 399 AA; 44764 MW; 790568 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 2: FILING DATE: 15-AUG-1988 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 483,913
FILING DATE: 22-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 422,613
FILING DATE: 17-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 20-AUG-1990 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 315,342 FILING DATE: 23-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: PITCHER, EDMUND REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                 399 amino acids
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                                                                                                                                STANDARD;
                          US/08447570
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Pred. No. 2.06e+00;
12; Mismatches 22; Indels
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 PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 23
APPLICATION NUMBER: US 23
APPLICATION NUMBER: 15-AUG-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 8: FILING DATE: 20-DEC-1991 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 8:
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APPLICANT:
                                                                                                                                                                                                            FILING DATE: 22-FEB-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                     FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 5:
FILING DATE: 07-SEP-1990
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FILING DATE: 21-NOV-
PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
FILING DATE: 04-DEC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                      FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 08-APR-
                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 22-FEB-
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TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33
                                                                                                                                                                     PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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 ELECOMMUNICATION INFORMATION:
                                                                                                                                           APPLICATION NUMBER: US 3: FILING DATE: 23-FEB-1989
                                                                                                                                                                                  APPLICATION NUMBER: US 4: FILING DATE: 17-OCT-1989
                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 569,920 FILING DATE: 20-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 18-OC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 04-DEC
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               REFERENCE/DOCKET NUMBER:
                          REGISTRATION NUMBER:
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OZKAYNAK, ENGIN
KUBERASAMPATH, THANGAVEL
RUEGER, DAVID C.
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IBM PC compatible
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04-DEC-1990
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                        27,829
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Matches 24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  194 GPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRS 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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LENGTH: 399 amino acid
                                             REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRITELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 667,274
FILING DATE: 11-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 752,764
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APPLICATION NUMBER: PC
FILING DATE: 19920311
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ADDRESSEE: TESTA HURWITZ & THIBEAULT
STREET: EXCHANGE PLACE 53 STATE STREET
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: OPPERMANN, HERMANN
APPLICANT: RUEGER, DAVID C
TITLE OF INVENTION: PROTEIN-INDUCED MORPHOGENESIS
                                                                                FILING DATE: 30-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release 1, 1999.
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                                                                                                                                                                                         FILING DATE: 19
CLASSIFICATION:
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TOPOLOGY: linear
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399 AA; 44764 MW; 790568 CN;
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AMINO ACID
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617/248-7100
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Query Match 1.4%;
Best Local Similarity 38.7%;
Matches 24; Conservative
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Local Similarity 38.7%;
                                                                                                          TELEFAX: (508) 435-695
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                 ZIP: v1/32
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DDS/MS-DOS
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MOLECULE TYPE: protein
UENCE 399 AA; 44764 MW; 790568 CN;
                                 TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 399 AA; 44764 MW; 790568 CN;
                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 399 amino acid
                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESq., EDMUND R.
REGISTRATION NUMBER: 27,829
                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: COHEN, CHARLES M.
TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                         REFERENCE/DOCKET NUMBER: CR
TELECOMMUNICATION INFORMATION:
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                                                                           TYPE:
                                                                                                                                                                                                                                                COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                          APPLICATION NUMBER: US/08/278,729A FILING DATE: 20-JUL-1994
                                                                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                                                                               CITY: HOPKINTON
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RUEGER, DAVID C.
PANG, ROY H.L.
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OZKAYNAK, ENGIN
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                                                                                                                                 (508) 435-9001
                                                                                                      d) 405
435-6951
NO: 23:
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Pred. No. 2.06e+00;
12; Mismatches 22
 Score 118; DB 1; Le
Pred. No. 2.06e+00;
12; Mismatches 22;
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Best Local
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/643,763A
FILING DATE: 06-MAY-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: FENTON ESG., GILLIAM M.
REGISTRATION NUMBER: 36,508
REGISTRATION NUMBER: 36,08
                                                                                                                                       SEQUENCE
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  254 LP 255
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                                                            12 GLALCALGGGHGPRPP-HTC-PQRRLG-ARERRDMQREILAVLGLPGR-PRPRAQPAAAR 67
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                                                                                                    Match 1.4%;
Local Similarity 38.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 399 AA; 44764 MW; 790568 CN;
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 399 amino acids
                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 248-7560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: MORPHOGENIC-I
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                       QP
                                              GPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRS 253
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                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
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                                                                                           Conservative
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                                                                                                                                                                                                                   7100
                                                                                        Score 118; DB 1;
Pred. No. 2.06e+00;
12; Mismatches 22
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ID US-07-901-703-13
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Best Local :
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                                                                                                   US-08-643-563A-23
                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 399 AA; 44764 MW; 790568 CN;
                                Sequence 23, Application US/08643563A
                                                                              XXXXXX
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Sequence 23, Application US/08643563A Patent No. 5707810
                                                                                                                                              254 LP 255
                                                                                                                                                                                        194 GPPLYQLGAATQARPPPHASGPRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRS 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13, Application US/07901703 Patent No. 5344654
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                                                                                                                                                                   68 QP 69
                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: STK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: PROSTHETIC DEVICES HATTITLE OF INVENTION: OSTEOGENIC PROPERTIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US FILING DATE: 19920616 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                        LENGTH:
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                                                                                                                                                                                                                                   Similarity 24; Conser
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llarity 38.7%;
Conservative
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EXCHANGE PLACE, 53 STATE STREET
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OZAKAYNAK, ENGIN
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KUBERASAMPATH, THANGAVEL
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                                                                                                    STANDARD;
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Pred. No. 2.06e+00;
12; Mismatches 22;
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GENERAL INFORMATION:

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Best Local :
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                                                                                                                  Sequence 10, Application US/08479666
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                                                                                              Sequence 10, Application US/08479666
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Local Similarity 38.78;
les 24; Conservation
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                                                                        GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 399 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: TWOMEY ESQ., MICHAEL J.
REGISTRATION NUMBER: 38,349
REFERENCE/DOCKET NUMBER: CRP-058CN2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 435-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein JENCE 399 AA; 44764 MW; 790568 CN;
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TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD
                                                             APPLICANT:
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TITLE OF INVENTION:
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                                                   OPPERMANN, HERMI
OZKAYNAK, ENGIN
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OZKAYNAK, ENGIN
                             RUEGER, DAVID C.
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       PANG, ROY H.L.
COHEN, CHARLES M.
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OP3-INDUCED MORPHOGENESIS
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Pred. No. 2.06e+00;
12; Mismatches 22; Indels
                                          THANGAVEL
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Best Local Similarity 38.7%;
Matches 24; Conservative
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                                                                                                                                                                                                                             Sequence 23, Application US/08155343A
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                                                                                                                                                                             Sequence 23, Application US/08155343A Patent No. 5656593
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 399 amino acids
                                                                                                                                                                                                                                                                                                                                                                 68 QP 69
                                                                                                                                                                                                                                                                                                                                                                                                             12 GLALCALGGGHGPRPP-HTC-PORRLG-ARERRDMOREILAVLGLPGR-PRPRAOPAAAR 67
                                                                                                                                  APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,666
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                  NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: FENTON ESG., GILLIAN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-
TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
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                                                                                                  TITLE OF INVENTION: MORPHOGENIC-INDUCED PERIODONTAL TISSUE TITLE OF INVENTION: REGENERATION.
                                                                                                                         APPLICANT: COHEN, CHARLES APPLICANT: PANG, ROY H.L.
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TOPOLOGY:
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ZIP: 01748
             COUNTRY: U
ZIP: 01748
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OPPERMANN, HERMAN
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                                                                                                                                     CHARLES M.
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pred. No. 2.06e+00;
12; Mismatches 22
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Local Similarity 38.7%;
local Similarity 38.7%;
les 24; Conservative
APPLICATION NUMBER: PCT/US93//
FILING DATE: 1930729
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: KELLEY, ROBIN D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: CRP-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (617) 248-7100 INFORMATION FOR SEQ ID NO: 23:
                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: RE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/155,343A
FILING DATE: 15-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 399 amino acid
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ATTORNEY/AGENT INFORMATION:
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TYPE: amino acid
TOPOLOGY: linear
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COMPUTER: II
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35 SOUTH STREET
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: 33
                                                                                             PCT/US93/07231
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Pred. No. 2.05e+00;
12; Mismatches 22;
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12 GLALCALGGGHGPRPP-HTC-PQRRLG-ARERRDMQREILAVLGLPGR-PRPRAQPAAAR 67 | :| || :| :| :| :| :| :|:
                                                                                                                                           NAME: A-REGISTRATION NUMBER: STK-REFERENCE/DOCKET NUMBER: STK-TELECOMMUNICATION INFORMATION: 617/248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        y Match 1.4%;
Local Similarity 38.7%;
hes 24; Conservative
                                         Match 1.48;
Local Similarity 38.78;
                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 399 amino acid
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                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
UENCE 399 AA; 44764 MW; 790568 CN;
                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05446
FILING DATE: 19930608
                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMU
REGISTRATION NUMBER: 27,
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LENGTH: 399 amino acid
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35 South Street
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                                  12; Mismatches 22; Indels
                                          Score 118; DB 2;
Pred. No. 2.06e+00;
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Pred. No. 2.06e+00;
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          Query Match 1.4%;
Best Local Similarity 38.7%;
Matches 24; Conservative
                                                 SEQUENCE
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                                                                                                       TELEPHONE: (508)435-9001
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10520
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 399 amino acid
                                                                                                                          NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-076PC
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                           APPLICATION NUMBER: US 07/923,780 FILING DATE: 31-JUL-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 0 FILING DATE: 11-MAR-1991 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: OP NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                              FILING DATE: 31-JUL-1992
ATTORNEY/AGENT INFORMATION:
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                                                MOLECULE TYPE: protein
ENCE 399 AA; 44764 MW; 790568 CN;
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                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/753,059 FILING DATE: 30-AUG-1991
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                                                                  TOPOLOGY:
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45 SOUTH STREET
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                  Score 118; DB 2;
Pred. No. 2.06e+00;
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Sequence 23, Application US/08462623
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                                                                                                                  68 QP 69
                                                                                                                                                                                   Match 1.4%;
Local Similarity 38.7%;
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CORRESPONDENCE ADDRESS:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
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Sequence 23, Application PC/TUS9307190
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                    12 GLALCALGGGHGPRPP-HTC-PQRRLG-ARERRDMQREILAVLGLPGR-PRPRAQPAAAR
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTED: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: CREATIVE BIOMOLECULES, INC 35 SOUTH STREET
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Pred. No. 2.06e+00;
12; Mismatches 22;
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Best Local Similarity 38.7%;
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                                    Sequence 8, Application PC/TUS9307189
                                                                                                       PCT-US93-07189-8
                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 23, Application US/08462623 Patent No. 5739107 GENERAL INFORMATION:
Sequence 8, Application PC/TUS9307189 GENERAL INFORMATION:
                                                                                                                                                    254 LP 255
                                                                                                                                                                                                 194 GPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRS 253
                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/445,8
FILING DATE: 22-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FENTON ESG., GILLIAN M.
REGISTRATION NUMBER: 36,508
                                                                                                                                                                            68 QP 69
                                                                                                                                                                                                                       12 GLALCALGGGHGPRPP-HTC-PQRRLG-ARERRDMQREILAVLGLPGR-PRPRAQPAAAR 67
                                                                                                                                                                                                                                                                                                                                       TELEFAX: (508) 435-6951
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 399 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
UENCE 399 AA; 44764 MW; 790568 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANAL MORPHUS
TITLE OF INVENTION: MORPHUS
TITLE OF INVENTION: ULCERS.
33
                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: CRP-074CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 435-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: UZIP: 01748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: HOPKINTON STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES STREET: 45 SOUTH STREET
                                                                                                                                                                                                                                               24;
                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPPERMANN, HERMANN
PANG, ROY H.L.
OZKAYNAK, ENGIN
SMART, JOHN E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COHEN, CHARLES M.
CHARETTE, MARC F.
KUBERASAMPATH, THANGAVEL
RUEGER, DAVID C.
                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MORPHOGEN TREATMENT OF GASTROINTESTINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US 08/445,882
                                                                                                                                                                                                                                               12; Mismatches
                                                                                                                                                                                                                                                        Score 118; DB 1;
Pred. No. 2.06e+00
                                                                                                       PRT;
                                                                                                       399 AA.
                                                                                                                                                                                                                                               22;
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Search completed: Fri Dec 18 18:31:03 1998 Job time : 32 secs.

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                                                                                                   Query Match 1.4%;
Best Local Similarity 38.7%;
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                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: KELLEY, ROBIN D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: CRP-
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 399 anino acids
                                             194 GPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRS 253
  254 LP
                       68 QP 69
                                                             12 GLALCALGGGHGPRPP-HTC-PQRRIG-ARERRDMQREILAVLGLPGR-PRPRAQPAAAR 67
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA: APPLICATION NUMBER: PC
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                         TYPE: ami
                                                                                                                                                                                                                                                                                             FILING DATE: 1
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: PATENT ADMINISTRATOR/CREATIVE BIOMOLECULES ADDRESSEE: INC. STREET: 35 SOUTH STREET CITY: HOPKINTON
                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U. ZIP: 01748
                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: MA
  255
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                                                                                                                                                                    de in 399 amino acids amino acid
                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOVEL MORPHOGENIC PROTEIN COMPOSITIONS OF MATTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23
                                                                                                    Score 118; DB 2;
Pred. No. 2.06e+00;
                                                                                                                                                                                                                                                                                                                    PCT/US93/07189
                                                                                         12;
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                                                                                          Mismatches
                                                                                          22;
                                                                                                              Length 399
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Fri Dec 18 18:31:23 1998; MasPar time 55.03 Seconds 793.597 Million cell updates/sec

Title:

Description: Perfect Score: (1-1154) from US08951733.pep 8624 1 HASGORCUTTOTION

Sequence: HASGQRCVLLRTWEALAPAT......TALEAAANPALPSDFKTILD 1154

Scoring table: PAM 150 Gap 11

Searched: 321025 seqs, 37841481 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-pending 1:P9 2:U60 3:U7 4:U80 5:U81 6:U82 7:U83 8:U84 9:U85 10:U86 11:U87 12:U88 13:U89 14:U90 15:U91 16:NEWP 17:NEWU6 18:NEWU8 19:NEWU9

Statistics: Mean 40.459; Variance 196.267; scale 0.206

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		•						
Result No.	Score	Query Match	Length	BB	IJ	Description		Pred. No.
1	8624	100.0	1154	13	US-08-951-	Sequence 20, F	Applicati	0.00e+00
2	8607	99.8	1189	18		Ψ	Applicat	0.00e+00
ω	8607	99.8	1189	3	US-08-911-	~	Applicati	0.00e+00
4	8607	99.8	1189	13	US-08-912-	-	Applicat	0.00e+00
U	8607	99.8	1200	18	US-08-974-	-	Applicat	0.00e+00
0	8607	99.8	1200	13	US-08-912-	•	Applicat	0.00e+00
7	8607	99.8	1200	ü	us-08-911-	33, 1	Applicati	0.00e+00
8	8607	99.8	1285	18	US-08-974-	Sequence 600,	Applicat	0.00e+00
9	8607	99.8	1285	13	US-08-911-	•	Applicati	0.00e+00
10	8607	99.8	1285	ü	us-08-912-	-	Applicat	0.00e+00
11	8590	99.6	1407	13	US-08-911-	55,	Applicati	0.00e+00
12	8590	99.6	1407	18	US-08-974-	628,	Applicat	0.00e+00
13	8590	99.6	1407	<u>1</u>	US-08-912-	Sequence 334,	Applicat	0.00e+00
14	8465	98.2	1132	18	US-08-974-	'n	Applicatio	0.00e+00
15	8465	98.2	1132	13	US-08-912-	,	Applicatio	0.00e+00
16	8465	98.2	1132	13	US-08-911-	2,	Applicatio	0.00e+00
17	8465	98.2	1132	14	US-09-042-	Sequence 3, Ap	Applicatio	0.00e+00
18	8465	98.2	1132	14	US-09-052-	2,	pplicatio	0.00e+00
19	8465	98.2	1132	12	US-08-854-	Sequence 225,	Applicat	0.00e+00
20	8465	98.2	1154	13	US-08-912-	323,	Applicat	0.00e+00
21	8465	98.2	1154	18	US-08-974-	•	Applicat	0.00e+00

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45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence		Seguence		Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence		Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	
603, Applicat			319, Applicat	 Applicati 	46, Applicati	602, Applicat	316, Applicat	101, Applicat	101, Applicat	101, Applicat	267, Applicat	47, Applicati	Applicatio	217, Applicat	217, Applicat	336, Applicat	77	Applicati	Applicatio	14, Applicati	344, Applicat	 Applicatio 	45, Applicati	
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ALIGNMENTS

RESULT US-08-951-733-20 STANDARD; PRT; 1154 AA.

Sequence 20, Application US/08951733

Sequence 20, Application US/08951733 GENERAL INFORMATION: APPLICANT: Harrington, Lea A.
APPLICANT: Robinson, Murray O.
TITLE OF INVENTION: NOVEL GENES ENCODING TELOMERASE PROTEINS
NUMBER OF SEQUENCES: 44 CORRESPONDENCE ADDRESS: STREET: One Amgen Co ADDRESSEE: One Amgen Center Drive Amgen Inc.

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy STATE: CA COUNTRY: USA ZIP: 91320-1789

APPLICATION NUMBER: US/08/951,733 FILING DATE: 16-OCT-1997

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/873,039
FILING DATE: 11-JUN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/751,189
FILING DATE: 15-NOV-1996
FILING DATE: 15-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Oleski, Nancy A.
REGISTRATION NUMBER: 34,688
REFERENCE/DOCKET NUMBER: A-433B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (805) 447-6504
TELEFAX: (805) 49-8011
INFORMATION FOR SEQ ID NO: 20:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1154 amino act
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1154 amino
TYPE: amino acid
STRANDEDNESS: unkno
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WLRRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTTFQKNRLFFYRK
                                                                                                                                                                                                                                                                                                                                                                                                    FGFALLDGARGGPPEAFTTSVRSYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCAL
                                                             FKSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAV
                                                                                                      VVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVR
                                                                                                                                                                                         SVWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDY
                                                                                                                                                                                                                                                                                      WQVYGFVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCA
                                                                                                                                                                                                                                                                                                                    NHAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSP
                                                                                                                                                                                                                                                                                                                                NHAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSP
                                                                                                                                                                                                                                                                                                                                                              EQLRPSFLLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLG
                                                                                                                                                                                                                                                                                                                                                                        EQLRPSFLLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FVLVAPSCAYQVCGPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HASGQRCVLLRTWEALAPATPAMPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRL
                                                                                                                           AQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKA 780
                                                                                                                                                 YVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVR
                                                                                                                                                                                                                                   WLRRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRK
                                                                                                                                                                                                                                                                           WQVYGFVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCA
HAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1154;
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Similarity 100.0%;
154; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
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Pred. No. 0.00e+00;
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GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Linguer, Joachim
APPLICANT: Nakamura, Toru
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Nakamura, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Ca
NUMBER OF SEQUENCES: 726
CORRESPONDENCE ADDRESS:
       APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
                                                                                                                    PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                        CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
US
                                                                                                              FILING DATE: 18-APR-PRIOR APPLICATION DATA:
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                                                                                                                                                            APPLICATION NUMBER: US 08/724,643 FILING DATE: 01-OCT-1996
                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 19-NOV
                                                                                                                                                                                                                                                                              MPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                 STREET:
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                                                                                                                                                                                                                                                                                                                          San Francisco
: California
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  08/911,312
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INFORMATION FOR SEQ ID NO: 61
SEQUENCE CHARACTERISTICS:
SERVICE CHARACTERISTICS:
1.ENGTH: 1189 amino acids
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FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: APPLE, RANDOLPH TEC
REGISTRATION NUMBER: 36,429
REGISTRATION NUMBER: 36,429
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
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LOCATION: 1.1189
OTHER INFORMATION: /n:
OTHER INFORMATION: me
OTHER INFORMATION: hT
ENCE 1189 AA; 133179 M
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                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
QVYGFVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAW
                                                                                                                                                                                                           GARRRGGSASRSLPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPA 336
                                                                                                                                                                                                                                                             VLVAPSCAYQVCGPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAP
                                                                                                                                                                                                                                                                                                               GFALLDGARGGPPEAFTTSVRSYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALF
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                                                                                                      QLRPSFLLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGN
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                                                                 HAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPW
                                                                                         QLRPSFLLSSLRPSLTGARRLYETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGN
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REFERENCE/DOCKET NUMBER: 015389-002610US
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Conservative
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Pred. No. 0.00e+00;
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                                                                                                                                             Sequence 34, Application US/08911312 GENERAL INFORMATION:
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                                                      APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William
TITLE OF INVENTION: Telomerase Re
NUMBER OF SEQUENCES: 170
                       NUMBER OF SEQUENCE ADDRESS:
CORRESPONDENCE ADDRESS:
Townsend and Townsend
Townsendero Center, J
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STREET:
CITY: Sa
STATE: C
COUNTRY:
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                   San Francisco
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 California
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Query Match
Best Local
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FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: US 08/915,503
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
ATTORNEY/AGENT INFORMATION:
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SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
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PRIOR APPLICATION DATA:
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                                                                                                      ASTQRCVLLRTWEALAPATPAMPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLV
EEATSLEGALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKHELYSSGDKE
                                           GARRRGGSASRSLPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPA
                                                           GARRRGGSASRSLPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPA
                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino a
STRANDEDNESS:
TOPOLOGY: lir
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OPERATING SYSTEM:
SOFTWARE: Patent:
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REFERENCE/DOCKET NUMBER: 015389-002500US
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Similarity 99.9%;
                                                                                                                                                                                                                                                                                                                                                                                                             LE TYPE: protein
1189 AA; 133179 MW; 7256545 CN;
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SYSTEM: PC-DOS/MS-DOS
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18-APR-1997
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NO: 34:
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Pred. No. 0.00e+00;
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                                                                                                                                               Sequence 325, Application US/08912951
  Sequence 325, Application US/08912951
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Linguer, Joachim
APPLICANT: Nakamura, Toru
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Best Local :
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STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
MOLECULE TYPE: protein
7-0-68607; DB
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                                                                                                                              Local
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CLASSIFICATION: 435
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APPLICANT:
APPLICANT:
TITLE OF IN
                                                                                                                                                                                                                                                            NAME: Apple, Randolph T.9
REGISTRATION NUMBER: 36.429
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
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LENGTH: 1189 amino aci
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APPLICATION NUMBER: I
FILING DATE: 01-OCT-
CLASSIFICATION: 435
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TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC
TITLE OF INVENTION: THERAPEUTIC METHODS
                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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                              ASTQRCVLLRTWEALAPATPAMPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLV
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           GFALLDGARGGPPEAFTTSVRSYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALF
                                                                          ASGQRCVLLRTWEALAPATPAMPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLV
APPLICATION NUMBER: US 08/844,419 FILING DATE: 18-APR-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/846,017 FILING DATE: 25-APR-1997 CLASSIFICATION: 435
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: San Francisco
STATE: California
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                                                                                                                               Similarity
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Harley, Calvin
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                                 GAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAA
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RESULT ID U

US-08-974-549-612

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Sequence 612, Application US/08974549 GENERAL INFORMATION:
INFORMATION FOR SEQUENCE CHARA
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APPLICANT:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
ADDRESSEE: Townsend Center, Eighth Floor
                                                                                                               FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
                                         REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Teneres 36,
                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 01
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 09-MAY-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOETWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
                                                                                                                                                            FILING DATE: 14-AUG-
PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
FILING DATE: 14-AUG-
PRIOR APPLICATION DATA:
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CLASSIFICATION:
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FILING DATE: 19-NOV-1997
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STATE: California
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N FOR SEQ ID NO:
CHARACTERISTICS:
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Chapman, Karen B.
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14-AUG-1997
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06-MAY-1997
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NAME/KBY: Protein
LOCATION: 1.1200
OTHER INFORMATION: /n
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MOLECULE TYPE:
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 KSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVR
                                                  VGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRA
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and Anti-Xpress tags, enterokinase
cleavage site and full length hTRT
protein"
2 MW; 7387257 CN;
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                                                                                                                                      APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAX-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Two Emparcanc
CITY: San Francisco
STATE: California
COUNTRY: United State
                             APPLICATION NUMBER: US 0: FILING DATE: 06-MAY-1997 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: TITLE OF INVENTION: THERAPEUTIC METHODS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   United States
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Harley, Calvin
Andrews, William H.
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Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lingner, Joachim
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  US 08/846,017
                                                                                                                  08/851,843
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Best Local Similarity 99.9%;
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NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 0153/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 324:
SEQUENCE CHARACTERISTICS:
LENGTH: 1200 amino acids
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                   VWSKLQSIGIRQHLKRYQLRELSEAEVRQHREARPALLISRLREIPKPDGLRPIVNMDYV
                                                                                                                                               LRRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GFALLDGARGGPPEAFTTSVRSYLPNTYTDALRGSGAWGLLLRRVGDDVLVHLLARCALF
                                                                                                                                                                                                                                                            QVYGFVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAW
                                                                                                                                                                                                                                                                                                                                                                     HAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                          QLRPSFILSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QLRPSFLLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGN
     VWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYV
                                                                                                                                                                                                                              QVYGFVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VLVAPSCAYQVCGPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAP
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                                                                                                                     LRRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKS
                                                                                                                                                                                                                                                                                                                                           HAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPW
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TOPOLOGY: 11
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CLASSIFICATION:
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V: 435
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Pred. No. 0.00e+00;
0; Mismatches 1;
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          SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/911,312
                                                                                                                                                                                            APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William
TITLE OF INVENTION: Telomerase Reverse Transcriptase
                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRA
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                                                                                              COUNTRY: USA
ZIP: 94111-3834
                                                                                                                      CITY: San Francisco
STATE: California
                                                                                                                                             STREET:
                                                                                                                                                          ADDRESSEE:
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                                                                                                                                             E: Townsend and
Two Embarcadero
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 14 - AUG - 1997
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 422
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 33
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US 08/
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 06-MAY-1997
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/
FILING DATE: 18-APR-1997
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ATTORNEY/AGENT INFORMATION:
NAME: Einhorn, Gregory P
                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 06-MAY-
PRIOR APPLICATION DATA:
                                                                                                                                                                       GARRRGGSASRSLPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPA
                                                                                                                                                                                                                                                                   GFALLDGARGGPPEAFTTSVRSYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALF
                                                                                                                                                                                                                                                                                                                      QRGDPAAFRALVAQCLVCVPWDARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAF 167
                                                                                                                                                                                                                                                                                                                                                                      ASTQRCVLLRTWEALAPATPAMPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLV 107
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 HAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPW
             HAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPW
                                                  QLRPSFLLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGN
                                                               QLRPSFLLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGN
                                                                                                                                                    GFALLDGARGGPPEAFTTSVRSYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALF
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FILING DATE: 14-AUG-1997
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09-MAY-1997
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Sequence 600, Application US/08974549
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APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Harley, Calliam H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 726
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAA 1187
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Best Local Similarity
Matches 1152; Conse
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FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION NUMBER: US 08/854,050
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08 /**
FILING DATE: 1/ 
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                                                                                                                                                                                                                               NAME/KEY: Protein LOCATION: 1..1285 OTHER INFORMATION: /n OTHER INFORMATION: en OTHER INFORMATION: th IENCE 1285 AA; 143529 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1285 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Apple, Randolph Ted REGISTRATION NUMBER: 36,429 REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT IMPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/915,503 FILING DATE: 14-AUG-1997 PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/844,419
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                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                  ASTQRCVLLRTWEALAPATPAMPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLV 192
                                         ASGORCVLLRTWEALAPATPAMPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 19
CLASSIFICATION:
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                                                                                                                                  Score 8607; DB 18;
Pred. No. 0.00e+00;
0; Mismatches 1;
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APPLICANT:
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APPLICANT:
APPLICANT:

Lingner, Joachim Nakamura, Toru Chapman, Karen B. Cech, Thomas R.

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US-08-974-549-600

STANDARD;

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GARRRGGSASRSLPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPA 432
                                              GAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAA 1272
                                                                                                       NIYKILLLQAYRFHACVLQLPFHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAK 1212
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                              GAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAA
                                                                                       NIYKILLLQAYRFHACVLQLPFHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAK
                                                                                                                                                 LEVQSDYSSYARTSIRASLTFNRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCT
                                                                                                                                                                                                        AKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRT
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                                          TELEFAX: (415) 576-030
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/911,312
FILING DATE: 14-AUG-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                        FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08,
FILING DATE: 06-MAY-1997
                                                                                    NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William
TITLE OF INVENTION: Telomerase
NUMBER OF SEQUENCES: 170
                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                         PRIOR APPLICATION DATA:
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ZIP: 941
                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 14-AUC
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                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
 TYPE: amino acid
STRANDEDNESS:
                              LENGTH:
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Nakamura, Toru
Chapman, Karen B.
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                                                                                                                                                                                                         US 08/912,951
14-AUG-1997
                                                                                                                                                                                                                                                                                                           UMBER: US 08/851,843
06-MAY-1997
                                                                                                                                                                              UMBER: US 08/915,503
14-AUG-1997
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LEVQSDYSSYARTSIRASLTFNRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCT 1152
                                                                                                                   KSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVR 972
                                                                                                                                                                            QDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAF 912
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                                                                                                                                                                                                                                                                                                                       LRRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTTPQKNRLFFYRKS
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                      AKTFLRTLYRGYPEYGCYVNLRKTYVNFPYEDEALGGTAFYQMPAHGLFPWCGLLLDTRT 1092
                                                                   IRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTH 1032
                                                                                                                                                                                                                                                                                                           LRRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKS
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                                                                                                                                                                 QDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAF
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Similarity 99.9%;
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TITLE OF INVENTION: THERAPEUTIC METHODS

APPLICANT: Morin, Greey B.
APPLICANT: Morin, Greey B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: THERAPEUTIC METHODS

TITLE OF SEQUENCES: 335
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                                                                                                PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/854,05
FILING DATE: 09-MAY-1997
CLASSIFICATION : 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,84
FILING DATE: 06-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/846,01
FILING DATE: 25-APR-1997
FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                               APPLICATION NUMBER: US 0
FILING DATE: 18-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAA 1272
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                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 14-AUG
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APPLICATION NUMBER: US 0 FILING DATE: 01-OCT-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                   COUNTRY: United States of America
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14-AUG-1997
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                       US 08/724,643
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Center, 8th Floor
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Matches 115
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SEQUENCE 1285 AA;
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REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 0153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 314:
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                                         QDPPPELYFYKYDVTGAYDTIPQDRLTEVIASIIKPQNTYCYRRYAVVQKAAHGHYRKAF
                                                                                           VGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRA
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KSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVR
                         QDPPPELYFVKVDVTGAYDT IPQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAF
                                                                             VGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRA
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                                                    APPLICATION NUMBER: US/08/
FILING DATE: 14-AUG-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Greeg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William
TITLE OF INVENTION: Telomerase Reverse Transcriptase
NUMBER OF SEQUENCES: 170
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

ADDRESSEE: Townsend and Townsend and Crew LLP
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                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
     APPLICATION NUMBER: US 08/846,017 FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Two Embarcae
CITY: San Francisco
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14-AUG-1997
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                                                                                                               08/844,419
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Best Local Similarity 99.7%;
Matches 1150; Conservative
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REFERENCE/DOCKET NUMBER: 015389-002500US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 55:
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APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
ATTORNEY/ACENT INFORMATION:
NAME: Einhorn, Gregory P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 1407 AA; 157668 MW;
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APPLICATION NUMBER: US 0
FILING DATE: 14-AUG-1997
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APPLICATION NUMBER:
FILING DATE: 06-MAY-
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1407 amino acids
                                                                        LRRSPGVGCVPAAEHRLREEILAKFLHWIMSVYVVELLRSFFYVTETTFQKNRLFFYRPS
                                                                                                                                     HAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPW
                                                                                                                                                                                        QLRPSFLLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGN
                                                                                                                                                                                                                                                                                            GARRRGGSASRSLPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPA 554
                                                                                                                                                                                                                                                                                                                                             VLVAPSCAYQVCGPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAP 494
                                                                                                                                                                                                                                                                                                                                                                                              GFALLDGARGGPPEAFTTSVRSYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALF 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                QRGDPAAFRALVAQCLVCVPWDARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAF 374
                                                                                                                                                                                                                                          EEATSLEGALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKE
                                                                                                                                                                                                                                                                               GARRRGGSASRSLPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPA
                                                                                                                                                                                                                                                                                                                              VLVAPSCAYQVCGPPLYQLGAATQARPPPHASGPRRLGCERAWNHSVREAGVPLGLPAP
                                                                                                                                                                                                                                                                                                                                                                                GFALLDGARGGPPEAFTTSVRSYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALF 181
                                                                                                                                                                                                                                                                                                                                                                                                                                  QRGDPAAFRALVAQCLVCVPWDARPPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAF 121
VWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYV
                                                                                                                           HAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPW
                                                                                                                                                                           QLRPSFLLSSLRPSLTGARRLYETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGN
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1; Mismatches
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        STREET: Two Embarcadero Center, Eic
STATE: San Francisco
STATE: California
COUNTRY: USA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATLING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
                                                                                                                          APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Harley, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 726
CORRESPONDENCE ADDRESS:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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CURRENT APPLICATION DATA:
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                                                                                                                     ADDRESSEE: Townsend and
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FILING DATE: 01-OCT-1997
ATTORNEY,AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE,DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 628:
                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                    255
  122
                          375
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EFILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION UNWBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNWBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION UNWBER: WO PCT/US97/176
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08,
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1407 amino acids
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APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                               INAME/KEY: Protein
LOCATION: 1.1407
OTHER INFORMATION: /n
OTHER INFORMATION: en
OTHER INFORMATION: 5/
OTHER INFORMATION: hT
OTHER INFORMATION: hT
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APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-PRR-1997
PRIOR APPLICATION DATA:
                                                                                                                       ASTORCVLLRTWEALAPATPAMPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLV 314
             GFALLDGARGGPPEAFTTSVRSYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALF 434
                                                                    QRGDPAAFRALVAQCLVCVPWDARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAF 374
                                                                                                         ASGQRCVLLRTWEALAPATPAMPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLV 61
 GFALLDGARGGPPEAFTTSVRSYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALF
                                                    QRGDPAAFRALVAQCLVCVPWDARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAF
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FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS:
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                                                                                                                                                              Conservative
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06-MAY-1997
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                                               GAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAA 1394
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  NPALPSDFKTILD
                                    GAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAA
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US-08-912-951-334

STANDARD;

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Best Local Similarity Matches 1150; Conser
                       Query Match
                                          MOLECULE TYPE:
SEQUENCE 1407 AA;
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                                                                                     TELEFAX: (415) 576-0301
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1407 amino acid
                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 18-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                   CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 06-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 25-APR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: HUMAN LECTHODS
TITLE OF INVENTION: THERAPEUTIC METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION NDATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                  APPLICATION NUMBER: US 00 FILING DATE: 01-OCT-1996 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                          NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
                                                                                                                                                   NAME: Apple, Randol REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0 FILING DATE: 14-AUG-1997
                                                                   STRANDEDNESS:
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HATLEY, CAIVIN
ANDREWS, WILLIAM H.
VENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC
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                                           MW; 10134798
      Score 8590; DB 13;
Pred. No. 0.00e+00;
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GAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAA 1394
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                       NIYKILLLQAYRFHACVLQLPFHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAK
                                                                                                                                AKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRT
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                                     NIYKILLLQAYRFHACVLQLPFHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAK
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GENERAL INFORMATION:
                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
                                              APPLICATION NUMBER: US 0 FILING DATE: 14-AUG-1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                APPLICATION NUMBER: US 0
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAX-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lingner, Joachim
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                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
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APPLICATION DATA:
                        APPLICATION NUMBER: WO PILING DATE: 01-OCT-1997
                                                                                                                                     FILING DATE:
                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/844,419 FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/0 FILING DATE: 19-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2, Application US/08974549
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Harley, Calvin B.
Andrews, William H.
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Chapman, Karen B.
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                                                                                                                                     14-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                           Release #1.0,
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                                                                                                            US 08/912,951
                                                                        US 08/915,503
                                     WO PCT/US97/17618
                                                                                                                                                US 08/911,312
 WO PCT/US97/17885
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INFORMATION FOR SEQ ID NO: 2:
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LENGTH: 1132 amino aci
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                                                                      RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI
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ATTORNEY/AGENT INFORMATION:
QETSPLRDAVVIEQSSSLNEASSGLEDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL
                        PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL
                                     PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL
                                                                                                                        LSEAEVROHREARPALLISRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLISRVKA
                                                                                                                                   LSEAEVROHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA
                                                                                                                                                                        LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE
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TOPOLOGY: linear
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REGISTRATION NUMBER: 36,429
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Similarity 100.0%;
132; Conservative
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US-08-912-951-2
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                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MX-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION OBTA:
APPLICATION DATA:
APPLICATION DATA:
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                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                        APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC
TITLE OF INVENTION: THERAPEUTIC METHODS
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cech, Thomas R. APPLICANT: Lingner, Joachim APPLICANT: Nakamura, Toru
                              APPLICATION NUMBER: US 0 FILING DATE: 06-MAY-1997 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: TWO
CITY: San I
STATE: Cali
COUNTRY: UR
ZIP: 94111
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APPLICATION NUMBER: FILING DATE: 25-APPLICATION: 43:
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United States
            25-APR-1997
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                       US 08/846,017
                                                                     08/851,843
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Best Local (
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REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 01536
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
            661
                                   623
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 01-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI
                                                                             VETIFIGSRPWMPGTPRRLPRLPORYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT
                                                                                                                                                                                                                                                                                                                                GAAPEPERTPYGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG
                                RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI
                                                                                                                                                    RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI
                                                                                                                                                                                                                                                                                  RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL
                                                                                                                                                                                                                                                                                                                   GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG
                                                                                                                                                                                                                                                                                                                                                                             ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR
                                                                                                                                                                                                                                                                                                                                                                                                            SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR
                                                                                                                                                                                                                                                                      RQHHAGPPSTSRPPRPWDTPCPPYYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL
                                                                                                                                                                                                                                                                                                                                                                 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR
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TOPOLOGY:
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Similarity 100.0%;
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1132 AA; 126995 MW;
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Pred. No. 0.00e+00;
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ΩY	683	683 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 7	742
8	721	-	780
Ϋ́	743	PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL E	802
용	781	•	840
Ϋ́	803	QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL	862
8	841		900
γQ	863	LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 9	922
g	901	-	960
Οy	923	RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 9	982
B	961	•	1020
Qy	983	NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIXKILLLQAYRFHACVLQLP	1042
В	1021		1080
γQ	1043	FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1	1102
В	1081	KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132	
νg	1103	KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1154	

Search completed: Fri Dec 18 18:34:40 1998 Job time : 197 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Fri Dec 18 18:17:21 1998; MasPar time 8.35 Seconds 804.709 Million cell updates/sec

Description: Perfect Score: Sequence: >US-08-951-733-14 (1-949) from US08951733.pep (1 of 2) 7113 1 HASGQRCVLLRTWEALAPAT.....PVEDEALGGTAFVQMPAHGL 949

Title:

Scoring table: PAM 150 Gap 11 77309 segs, 7078906 residues

Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-issued 1:5_COMB 2:PCT9_COMB 3:backfiles1

Statistics: Mean 36.658; Variance 177.719; scale 0.206

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 3 3 4 4 5 5 7 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
125 125 125 125 125 125 125 125 125 125	Score
	Query Match I
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Length D
222222111111121121111	DB
US-07-841 US-08-643 US-08-462 PCT-US93-0 US-08-206- US-08-206- US-08-206- US-08-206- US-08-480- US-08-480- US-08-481- US-08-643- US-08-643- US-08-479- US-08-479- PCT-US93-0 PCT-US93-0 PCT-US93-0 PCT-US93-0 PCT-US93-0	ID
Sequence 21 Sequence 29 Sequence 21	Description
Applicati	1 1 1 1 1 1 1 1
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1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7
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PCT-US93-0 PCT-US91-0	US-08-451-	US-08-406-	PCT-US93-0	US-08-480-	PCT-US93-0	PCT-US93-0	US-08-462-	PCT-US93-0	PCT-US93-1	PCT-US93-0	PCT-US93-0	US-08-155-	US-08-479-	000	us-07-901-	US-08-643-	US-08-278-	PCT-US92-0	US-08-447-	US-08-147-
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ALIGNMENTS

388888	88888	888888	88888	8888	88888	88888	88888	SXEX	DXXXX	RESULT
APPLICATION NUMBER: US 660,162 APPLICATION NUMBER: US 660,162 FILING DATE: 22-FEB-1991 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 621,988 APPLICATION NUMBER: US 621,988 FILING DATE: 04-DEC-1990	C-1991 A: US 827, N-1992 A:	CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/841,646 FILING DATE: 19920221 CLASSIFICATION: 530 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 810,560	MEDIUM TYPE: Floppy G15K COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25	B S	DENCE ADDRESS EE: TESTA, F 53 STATE ST BOSTON	APPLICANT: KUBEKASAMFATH, THANGAVEL APPLICANT: RUEGER, DAVID C. APPLICANT: PANG, ROY H.L. TITLE OF INVENTION: OSTEOGENIC DEVICES NUMBER OF SEQUENCES: 33	66683 RMATION: OPPERMANN, HERN OZKAYNAK, ENGIN	Sequence 29, Application US/07841646 Sequence 29, Application US/07841646	XXXXXX	LT 1 US-07-841-646-29 STANDARD; PRT; 402 AA.

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Best Local
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                              Sequence
                                                               XXXXXX
                                                                              US-08-643-763A-21
                                                                                                                                                                                                            SEQUENCE
        Sequence 21, Application Patent No. 5733878
                                                                                                                                            194 GPPLYQLGAATQA-RPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASR 252
                                                                                                              253 SLP 255
                                                                                                                                                                       1.8%;
Local Similarity 39.7%;
les 25; Conservation
GENERAL INFORMATION:
                                                                                                                              68 RLP 70
                                                                                                                                                            12 GLALCALGGGGPGLRPPP-GC-PQRRLG-ARERRDVQREILAVLGLPGR-PRPRAPPAAS 67
                                                                                                                                                                                                                                                         TELEFAX: 617/24 INFORMATION FOR SEQ
                                                                                                                                                                                                       MOLECULE TYPE: protein
JENCE 402 AA; 44698 MW; 800499 CN;
                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acid
                                                                                                                                                                                                                                                                                                     FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 4: FILING DATE: 17-OCT-1989 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 617/248-7000
                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 22-FEB-1990 PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 3 FILING DATE: 23-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 5' FILING DATE: 07-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 6 FILING DATE: 18-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-001CP6
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                              21, Application US/08643763A
                                                                                                                                                                                                                                  AMINO ACID
                                                                                                                                                                                                                                         402 amino acids
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                                                                                                                                                                                                                                                         ID NO:
                                                                              STANDARD;
                US/08643763A
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                                                          Patent No. 5/4107.

GENERAL INFORMATION:

SMART,
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APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: NUMBER OF SEQUENCES:
                        APPLICANT:
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                APPLICANT:
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Query Match 1.8%;
Best Local Similarity 39.7%;
Matches 25; Conservative
                                                                                                                                                                                                                                       Sequence 21, Application US/08451953A
                                                                                                                                                                                 Sequence 21, Application US/08451953A Patent No. 5741641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194 GPPLYQLGAATQA-RPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASR 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Relea
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/C
FILING DATE: 06-WAY-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (617) 248-710 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
JENCE 402 AA; 44764 MW; 803627 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: CR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION: NAME: FENTON ESq., GILLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: FENTON ESQ., GILLIAN M. REGISTRATION NUMBER: 36,508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                  KUBERASAMPATH, TH
RUEGER, DAVID C.
PANG, ROY H.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45 SOUTH STREET
                                                                                                          OPPERMANN, HERMI
OZKAYNAK, ENGIN
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RUEGER, DAVID (
                                    COHEN, CHARLES M.
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248-7100
21:
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                                                                                                                                                JOHN
MORPHOGENIC PROTEIN SCREENING METHOD 33
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                                                                                                                             HERMAN
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Pred. No. 5.57e-01;
12; Mismatches 21
                                                                                          THANGAVEL
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Best Local Similarity 39.7%;
                                                                                                                                 Patent No. 5/3920.

GENERAL INFORMATION:
APPLICANT: COHEN, CHARLES M.
APPLICANT: CHARETTE, MARC F.
APPLICANT: KUBERASAMPATH, THANGAVEL
                                                                                                                                                                                                                                                                                                   US-08-462-623-21
                                                                                                                                                                                                                                                                             XXXXXX
                                                                                                                                                                                                                                Sequence 21, Application US/08462623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 01748

COMPOTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1

CURRENT APPLICATION DATA:

APPLICATION UNMBER: US/08/451,953A

FILING DATE: 26-MAY-1995
                                                                                                                                                                                                                                                                                                                                             253 SLP 255
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                                                                                                                                                                                                                                                                                                                                                                   68 RLP 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (508) 435-6951
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
                                                                                                                      APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
JENCE 402 AA; 44764 MW; 803627 CN;
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NAME: PITCHER ESG., EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (508) 435-9001
                                                    NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                          TITLE OF INVENTION: MORPHOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                         APPLICANT:
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STATE: M
COUNTRY:
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                                STREET:
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                                          ADDRESSEE:
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5. 5739107
                     HOPKINTON
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                                                                                               OPPERMANN, HERMANN
PANG, ROY H.L.
OZKAYNAK, ENGIN
SMART, JOHN E.
                                E: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES 45 SOUTH STREET
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                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                    MORPHOGEN TREATMENT OF GASTROINTESTINAL
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Best Local Similarity 39.7%;
Matches 25; Conservative
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MOLECULE TYPE: protein
SEQUENCE 402 AA; 44764 MW; 803627 CN;
                                                                                                                                                                                                                                                                                           Sequence 21, Application PC/TUS9308742
                                                                                                                                                                                                                                                                                                                                              XXXXXX
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                                                                                                                                                                                                                                                       Sequence 21, Application PC/TUS9308742 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 22-MAY-1995
ATTORNEY/AGENT INFORMATION:
                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: CREATIVE BIOMOLECULES, INC
STREET: 45 SOUTH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: FENTON ESQ., GILLIAN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-074CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 435-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                    TITLE OF INVENTION: MORPHOGEN-INDUCED PERIODONTAL TISSUE REGENERATION NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                     CLASSIFICATION:
                                   FILING DATE:
                                             APPLICATION NUMBER:
                                                                                                                                  COUNTRY: UI
                                                                                                                                                          STATE:
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                                               PCT/US93/08742
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Pred. No. 5.57e-01;
12; Mismatches 21;
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ATTORNEY/AGENT INFORMATION: NAME: KELLEY ESQ, ROBIN D

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Best Local S
Matches 2
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/027,070
FILING DATE: 04-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/841,646
FILING DATE: 21-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 1.8%;
Local Similarity 39.7%;
nes 25; Conservative
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INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/206,864
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: CRP-067
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7477
TELEFAX: 617/248-7100
                                                                                                                                                                                                                                                                                             APPLICANT: KUBERASAMPATH, THANGAVEL
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: RECOMBINANT OSTEOGENIC PROTEIN PRODUCTION
                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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CITY: HOPKINTON
STATE: MA
                                                                                                                                                                                    COUNTRY: US
ZIP: 01748
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45 SOUTH STREET
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JONES, WILLIAM K
TUCKER, RONALD F
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Pred. No. 5.57e-01;
12; Mismatches 21
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Best Local Similarity 39.7%;
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                                         COMPOTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/155,343A
FILING DATE: 15-NOV-1993
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FENTON ESG., GILLIAN M.
REGISTRATION NUMBER: GRP-067FW
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELEFAX: (617) 248-7100 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: MORPHOGENIC-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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TOPOLOGY:
                                  TELEPHONE:
                                                                                                                                                                                                            COUNTRY: USA
ZIP: 01748
                                                                                                                                                                                                                                  STATE: MA
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PANG, ROY H.L.
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                                  (617)
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                                   248-7560
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Pred. No. 5.57e-01;
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Best Local :
                                      Matches
                                               Query Match
Best Local :
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MOLECULE TYPE: protein
SEQUENCE 402 AA; 44764 MW; 803627 CN;
                                                                      TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE 402 AA; 44698 MW; 800499 CN;
                                                                                             TELEFAX: 61//2*, INFORMATION FOR SEQ ID NO: 21.
SEQUENCE CHARACTERISTICS:
SEQUENCE 402 amino acids
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       194 GPPLYQLGAATQA-RPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASR 252
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Local Similarity 39.7%;
hes 25; Conservativo
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                      12 GLALCALGGGGPGLRPPP-GC-PORRLG-ARERRDVOREILAVLGLPGR-PRPRAPPAAS 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 RLP 70
                                      Match 1.8%;
Local Similarity 39.7%;
les 25; Conservative
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07231
                                                                                                                           REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: CRITELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEPAX: 617/248-7100
                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                     ATTORNEY/AGENT INFORMATION: NAME: KELLEY, ROBIN D.
                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                               FILING DATE:
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                                      Score 125; DB 2;
Pred. No. 5.57e-01;
12; Mismatches 21
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Pred. No. 5.57e-01;
12; Mismatches 21
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US-08-480-528A-8
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194 GPPLYQLGAATQA-RPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASR 252
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                              12 GLALCALGGGGPGLRPPP-GC-PORRIG-ARERRDVQREILAVLGLPGR-PRPRAPPAAS 67
                                                                  y Match 1.8%;
Local Similarity 39.7%;
hes 25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                    MOLECULE TYPE: protein PROCE 402 AA; 44764 MW; 803627 CN;
                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: FENTON ESQ., GILLIAN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 248-7560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: PANG, ROY H.L.
APPLICANT: COHEN, CHARLES M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: MA
                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/480,528A FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: US
ZIP: 01748
                                                                                                                                                                       TOPOLOGY:
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45 SOUTH STREET
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                                                                  Score 125; DB 1; Leading Pred. No. 5.57e-01; 12; Mismatches 21;
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Sequence 29, Application US/08147023
Patent No. 5468845
GENERAL INFORMATION:
APPLICANT: OPERWANN, HERMANN
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAN
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nes 25; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: STK-057
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                             68 RLP 70
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/901,703
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APPLICANT: OPPERMANN, ENGIN
TITLE OF INVENTION: PROSTHETIC DEVICES HAVING ENHANCED
TITLE OF INVENTION: OSTEOGENIC PROPERTIES
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acid
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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ZIP: 02109
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OPPERMANN, HERMANN
OZKAYNAK, ENGIN
KUBERASAMPATH, THANGAVEL
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KUBERASAMPATH, THANGAVEL
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                                                                                                                                                                                          STANDARD;
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Pred. No. 5.57e-01;
12; Mismatches 21; Indels
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   TELEFAX: 617/24 INFORMATION FOR SEQ
                                           FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 579
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 569
FILING DATE: 20-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 61
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 51
FILING DATE: 18-OCT-1990
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APPLICATION NUMBER: US 62
FILING DATE: 04-DEC-1990
                                                                                                                                                                                       APPLICATION NUMBER: US 315,342 FILING DATE: 23-FEB-1989 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                             FILING DATE: 22-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 4
FILING DATE: 17-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 21-NOV-1990 PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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APPLICATION NUMBER: US 621,988
FILING DATE: 04-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 28-JAN-1992 PRIOR APPLICATION DATA:
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ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: 53 STATE STREET
                                                                                                                                             FILING DATE: 15-AUG-: PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                            TELEPHONE:
                                                                                                                APPLICATION NUMBER: US 1 FILING DATE: 08-APR-1988
                                                                                                                                                            APPLICATION NUMBER: US 232,630 FILING DATE: 15-AUG-1988
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                617/248-7100
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                              617/248-7000
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21-FEB-1992
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Best Local Similarity 39.7%;
Matches 25; Conservative
Query Match
                                                       SEQUENCE
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TOPOLOGY: linear
MOLECULE TYPE: protein
MOLECULE TYP
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                                                                                                                                          TELEFAX: (508) 435-6951
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
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NAME: TWOMEY ESG., MICHAEL J.
REGISTRATION NUMBER: 38,349
REFERENCE/DOCKET NUMBER: CRP-058CN2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET: 45 SOUTH STREET
                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD NUMBER OF SEQUENCES: 33
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                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/01 FILING DATE: 06-MAY-1996 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                  TELEPHONE:
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                                                    LE TYPE: protein
402 AA; 44764 MW; 803627 CN;
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amino acid
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                                                                                                                           amino acid
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                                                                                                    linear
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       1.8%; Score 125;
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  Length 402;
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Query Match 1.8%;
Best Local Similarity 39.7%;
Matches 25; Conservative
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                                               SEQUENCE
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FILING DATE: 20-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 752,857
FILING DATE: 30-AUG-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                   TELEFAX: (617) 248-710
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
APPLICANT:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                               FILING DATE: 11-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: OZKAYI
APPLICANT: RUEGEI
APPLICANT: PANG,
                                                         MOLECULE TYPE:
                                                                                                                                        TELEPHONE: (617) 248-7560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: RUEGER, DAVID C.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: TRANSHMENT TO PREVENT LOSS OF AND/OR
TITLE OF INVENTION: INCREASE BONE MASS IN METABOLIC BONE DISEASES
                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                       TOPOLOGY:
                                                                               LENGTH: 402 amino acids
TYPE: amino acid
                                                                                                                                                               REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CR
                                                                                                                                                                                      NAME: FENTON ESq., GILLIAN M.
                                                                                                                                                                                                                         APPLICATION NUMBER: US 667,274
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                                              LE TYPE: protein
402 AA; 44764 MW; 803627 CN;
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COHEN, CHARLES
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OZKAYNAK, ENGIN
                                                                     linear
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                                                                                                                             7) 248-7560
248-7100
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 Score 125; DB 1; Le
Pred. No. 5.57e-01;
12; Mismatches 21;
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                       Length 402;
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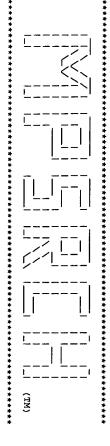
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                                                                             1.8%;
Local Similarity 39.7%;
nes 25; Conservation
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                     68 RLP 70
                                                             12 GLALCALGGGGPGLRPPP-GC-PQRRLG-ARERRDVQREILAVLGLPGR-PRPRAPPAAS 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 RLP 70
                                                                                                                                                                             TELEFAX: (508) 435-695
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                          MOLECULE TYPE: protein JENCE 402 AA; 44698 MW; 800499 CN;
                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/479,666
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                                                                                                                                                                                                              TELEPHONE: (508) 435-9001
                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: FENTON ESQ., GILLIAN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-076DV
                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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 SLP 255
                                          GPPLYQLGAATQA-RPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASR 252
                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 01748
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                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                     LENGTH:
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RUEGER, DAVID C.
                                                                                                                                                  linear
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                                                                                 Score 125; DB 1; Length 402, Pred. No. 5.57e-01; 12; Mismatches 21; Indels
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RESULT 15
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CC Sequence 21, Applic
CC Patent No. 5650276
CC Patent INFORMATI
CC PATENT SAME
CC APPLICANT: OPP
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CC APPLICANT: COMP
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CC CONTEXT: MA
CC COUNTAY: HOPKING
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  253 SLP 255
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INFORMATION FOR SEQ ID NO: 15
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
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                                                                                                                                          12 GLALCALGGGGPGLRPPP-GC-PQRRLG-ARERRDVQREILAVLGLPGR-PRPRAPPAAS 67
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NAME: PITCHER ESQ., EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-
TELECOMMUNICATION INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES STREET: 45 SOUTH STREET
                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein ENCE 402 AA; 44764 MW;
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                                                    RLP 70
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Similarity 39.7%;
25; Conservative
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OZKAYNAK, ENGIN
KUBERASAMPATH, THANGAVEL
RUEGER, DAVID C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       435-9001
                                                                                                                                                                                                            Score 125; DB 1;
Pred. No. 5.57e-01;
12; Mismatches 21
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Search completed: Fri Dec 18 18:17:43 1998 Job time: 22 secs.



Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

Run on: MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Fri Dec 18 18:10:34 1998; MasPar time 33.93 Seconds 954.989 Million cell updates/sec

Tabular output not generated.

>US-08-951-733-14 (1-949) from US08951733.pep (1 of 2) 7113

Description: Perfect Score: Sequence: 1 HASGQRCVLLRTWEALAPAT......PVEDEALGGTAFVQMPAHGL 949

Scoring table: PAM 150 Gap 11

Searched: 107076 segs, 34141958 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: pir56 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 53.200; Variance 116.643; scale 0.456

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

3 3 4 4 4 4 7 5 5 5 6 6 6 7 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
162 162 142 136 137 137 137 137 137 137 137 137 137 137	Score
PPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP	Query Match Length
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ALIGNMENTS

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271 LSHLSRQSPKER-VLKFIIVILQKLLPQEMFGSKKNKGKIIKNLNLLLSLPLNGYLPFDS 329 : : : : : :	LSHLSRQSPKER-V		8 B
4.4%; Score 314; DB 2; Length 884; 24.3%; Pred. No. 1.95e-30; 7ative 122; Mismatches 202; Indels 44; Gaps 37;	Query Match 4.4%; Best Local Similarity 24.3%; Matches 118; Conservative	Query Ma Best Loc Matches	
To SGD:EST2 ##cross-references SGD:S0004310; MIPS:YLR318w p_position 12R # #length 884 #molecular-weight 102662 #checksum 7604	#gene SGD:EST2 ##cross-references SGD #map_position 12R #map_position #m	#gene #gene #map_pc	დ 6
##INDIECULE_LYPE DNA ##residues 1-884 ##label DUZ ##cross-references EMBL:U20618; NID:g2258165; PID:g662136; MIPS:YLR318w ##experimental_source strain S288C (AB972)	##mulecute_ye wa ##residues 1 -884 ##label DUZ ##cross-references EMBL:U20618; N ##experimental_source strain S288	###CI ###CI ###IIC	o,
mence of S. cerevisiae cosmid 8543.	iption The sequence sion \$53396	#description #accession	
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hypothetical protein 1.6543.12 #formal_name Saccharomyces cerevisiae 05-May-1995 #sequence_revision 01-Sep-1995 #text_change 06-Feb-1998	NAMES	ALTERNATE ORGANISM DATE	DOD
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#journal Mol. Biol. Med. (1983) 1:21-45
#title Sequence analysis of the 17,166
Epstein-Barr virus.
#cross-references MUID:85035713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #contents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ts annotation; protein coding region
The sequence contains four perfect repeats (residues 149-273, 274-398, 399-523, and 524-648).
TION #superfamily human herpesvirus 4 BHLF1 protein
#length 660 #molecular-weight 66244 #checksum 8900
                                                                                                                                                                                                                                                                                                                                                                                                                             48;
        JC1306 #type complete
v1rion protein homolog - bovine herpesvirus 1
alpha TIF; BHV-I protein homolog; ICP25; Vmw65; VP16
#formal_name bovine herpesvirus 1
05-Mar-1993 #sequence_revision 05-Mar-1993 #text_change
09-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.; Hatfull, G.; Hudson, G.S satchwell, S.C.; Seguin, C.; Tuffnell, P.S.; Barrell, Nature (1984) 310:207-211

DNA sequence and expression of the B95-8 Epstein-Barr v
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BHLF1 protein - human herpesvirus 4 (strain B95-8)
#formal_name human herpesvirus 4, Epstein-Barr virus
25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change
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This protein interacts with cellular transcription factors to transactivate immediate early viral genes.
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##cross-references GB:X78052; NID:g459246; PID:g459248
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                                                                                                                                                                                               99 PLL-RPAAPNLTWSDDFVMDALATGRRIK 126
                                                                                                                                                                                                                                                                                                                         Match 2.0%;
Local Similarity 33.7%;
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                                                                                                                                                             RFIPKPDGLRPIVNMDYVVGA-RTFRREK 671
                                                                                                                                                                                                                                  VTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRV-QLRELSEAEVRQHREARPALLTSRL
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Similarity 31.3%;
46; Conservative
basic proline-rich protein IB-5; proline-rich peptide P-
#formal_name Homo sapiens #common_name man
19-Feb-1984 #sequence_revision 12-Apr-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Steibl, H.D.; Lewecke, F.M.
Gene (1995) 156:37-42
IS1222: analysis and distribution
in Enterobacter agglomerans 339
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Gene (1992) 119:259-263
Sequences of the bovine herpesvirus 1 homologue of herpes
simplex virus type-1 alpha-trans-inducing factor (UL48).
                                                   PIHUSD #type complete salivary proline-rich glycoprotein precursor PRB4 (large allele) - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein B (insertion sequence IS1222) -
Enterobacter agglomerans
#formal_name Enterobacter agglomerans
03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change
09-Sep-1997
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#molecular-weight 54028
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Pred. No. 3.83e-04;
23; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 153; DB 2;
Pred. No. 1.03e-05;
33; Mismatches 56
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#title
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#title
                                                                                                                                                                                                                                                                                                                                               #title Complete amino acid sequence of a basic proline-rich peptide.
P-D, from human parotid saliva.
#cross-references MUID:83186122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #journal
#title
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#journal Genetics (1988) 120:267-278
#title Length polymorphisms in human proline-rich
generated by intragenic unequal crossing
#cross-references MUID:89121440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #cross-references MUID:91190884
#accession E38355
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                                                                                                                          authors
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1-36, E',38-112,'T',114-115,'P',117-121,185-271,'A',
##residues 1-36, E',38-112,'T',114-115,'P',117-121,185-271,'A',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##cross-references EMBL:X07882; NID:g35647; PID:g296670
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                                                                                                                                                     ##molecule_type protein
##residues 54-57,'E',59-73,'R',82-101 ##label
                                                                                                                                                                                                                                                                                                ##molecule_type protein
##residues 241-310 ##label SAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##molecule_type protein
##residues 241-254,'KN',257-310 ##label KAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##residues 35-36,'E',38-112,155-310 ##cross-references EMBL:X07704
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##cross-references EMBL:X07715
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##molecule_type protein
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s03175
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$03176; $03175
$62891
                              Charlton, A.J.; Baxter, N.J.; Lilley, T.H.; H
McDonald, C.J.; Williamson, M.P.
FEBS Lett. (1996) 382:289-292
Tannin interactions with a full-length human
proline-rich protein display a stronger aff
single proline-rich repeats.
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Basic proline-rich proteins from human parotid saliva: relationships of the covalent structures of ten protfrom a single individual.
                                                                                                                                                                                                        Shimomura, H.; Kanai, Y.; Sanada, K.
J. Biochem. (1983) 93:857-863
Amino acid sequences of glycopeptides obtained from proline-rich glycoprotein of human parotid saliva.
                                                                                                                                                                                                                                                                                                                                                                                                         Saitoh, E.; Isemura, S.; Sanac
J. Biochem. (1983) 93:495-502
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##cross-references GDB:119514;
#map_position 12p13.2-12p13.2
#introns 22/1; 34/1
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#accession B24264
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                                                                                                                                                                                                                                                                                                                                 ##molecule_type DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     281 APPAGKPOGPPPPPOGGRPPRP 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  259 RPRRGAAPEPERTPVGQGSWAHPGRTRGPSDR-GFCVVSPARPAE-EATSLEGALSGTRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            221 HPGKPEGPPPQEGNKSRSARSPPGKPQGPPQQEGNKPQGPPPPGKPQGPPPPGGNPQQPQ 280
                                                                                                                                                                          y Match 1.9%;
Local Similarity 27.2%;
hes 41; Conservative
                                                                                                                           24 VNGSQQGPPPPGGPQPRPPQGPPPPGGPQPRPPQGPPPPGGPQPRPPQGPPPPGGPQPRP
                                         84 PQGPPPPGGPQQRP-PQGPPPPGGPQPRPPQGPPPPAGPQPPPPAGPHLRPTQG 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SHPSVGRQHHAGPPSTSRPPRP
PRRGAAPE-PERTPVGQGSWAHPG-RTRGPSDRGFCVVSPARPAEEATSLEGA-LSGTRH
                                                                                        LGAATQARPPPHASGPRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKR
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Similarity 28.2%;
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J. Biol. Chem. (1985) 260:15863-15872
The structure and organization of a pi
of a mouse multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B24264 #type fragment
proline-rich protein MP3 - mouse (fragment)
proline-mai_name Mus musculus #common_name house mouse
09-Sep-1987 #sequence_revision 09-Sep-1987 #text_cl
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#product proline-rich peptide P-D #status experin
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protein IB-5
it is unclear from the peptide sequence
a product of the PRB2 (PIR:PIHUPF) or
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                                                                                                                                                                          Score 136; DB 2; Le
Pred. No. 1.65e-03;
38; Mismatches 65;
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Pred. No. 2.85e-04;
41; Mismatches 52
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                                                                                                                                              ##molecule_type DNA
#residues 1-317 ##label ANN
##cross-references GB:M23236; GB:J03891; NID:g200535;
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##residues 1-316 ##label DEG
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Similarity 30.9%;
21; Conservation
                                                                                                                                                                                                                             Ann, D.K.; Smith, K.; Carlson, D.M.
J. Biol. Chem. (1988) 263:10887-10893
Molecular evolution of the mouse proline-rich protein
multigene family. Insertion of a long interspersed repeated
DNA element.
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homeotic
                                                                                #superfamily saliva
                                                                                                                                                                                                                                                                                                                                                  proline-rich protein M14 precursor - mouse
#formal_name Mus musculius #common_name house mouse
30-Jun-1989 #sequence_revision 30-Jun-1989 #text_c
20-Mar-1998
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DNA binding; homeobox; nucleus; transcription
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Nucleic Acids Res. (1991) 19:3742
Nucleotide seguence of a novel divenced a DNA binding protein.
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          *product proline-rich protein M14 *status predicted #label #label MAT
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Library, January 1991
rfamily unassigned homeobox proteins; homeobox homology
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Best Local Similarity 26.4%;
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#accession S019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##status preliminary
##molecule_type genomic RNA
##residues 1-628 ##label MOR
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                                                                                                                                                                                                             SYRHRRPYPLLPNPPAALPSIAYTSSRGKIHHSLPKGALPK-EGAPPPPRRL 442
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Similarity 25.08;
73; Conservation
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 S27923
S27923
                                                  $27923  #type complete
gene LF3 protein - human herpesvirus 4
#formal_name human herpesvirus 4, Epstein-Barr virus
19-Mar-1997  #sequence_revision 19-Mar-1997 #text_chan
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Pred. No. 5.19e-03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                ##molecule_type mRNA
##residues 1-227 ##label CLE
##cross-references GB:M11902; NID:9200544; PID:9200545
CLASSIFICATION #superfamily proline-rich protein
SUMMARY #length 227 #checksum 1378
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*coross-references MUID:86033799
*contents Clone rowrin
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#title
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##cross-references EMBL:M35547; NID:g330420; PID:g330421
# #length 924 #molecular-weight 94304 #checksum
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Local Similarity 28.28;
les 37; Conservative
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Local Similarity 27.3%;
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                                                                                 12
                                                                                                                                                              PPAGPQPRPPQ-GPPPTGPQPRPTQGP-PP 193
                                                                                                                                        HSHPSVGRQHHAGPPSTSRPPRPWDTPCPP 345
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                                                                                                                                                                                                                                                         GPPPPGGPQPRPPQGPPPPGG-PQPRPPQGPPPPPGGPQLRPPQGPPPPAGPQPRPPQGPP 165
                                                                                                                                                                                                                                                                                                QLGAATQARPPPHAS-GPRRRLGCE-RAWNHSVREAGVPLGLPAPGARRRGGSASRSLPL 256
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                                                                                                                                                                                                                   PKRPRRGAAPEPERTPYGQGSWAHPGRTRGPSDRGFCVVSPAR-PAEEATSLEGALSGTR 315
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Sequence and transcription of Raji Epstein-Barr virus DNA
spanning the B95-8 deletion region.
ORF4 protein - Orf virus (strain NZ2)
#formal_name Orf virus
23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change
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J. Biol. Chem. (1985) 260:13471-13477
Novel multigene families encoding highly repetitive peptide
sequences. Sequence analyses of rat and mouse proline-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proline-rich protein - mouse (fragment)
#formal_name Mus musculus #common_name house mouse
08-Mar-1989 #sequence_revision 08-Mar-1989 #text_ci
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                                            #type complete
in - Orf virus
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                                                                                                                                                                                                                                                                                                                                                                       Score 125; DB 2;
Pred. No. 3.67e-02;
34; Mismatches 67
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Best Local Similarity 28.2%;
Matches 33; Conservative
                                                                                                                                                         Matches
                                                                                                                                                                                           Query Match
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#title
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#journal Virology (1990) 176:379-389
#title Sequence analysis of the inverted terminal repetition in
genome of the parapoxvirus, orf virus.
#cross-references MUID:90266454
#accession D34768
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                                                                                                                                                                                                                               ##residues 1-14 ##label RO2
##coss references EMBL:X61126
IFICATION #superfamily proline-rich protein
#superfamily broilecular-weight 31129
RY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##residues 1-300 ##label ROB
##cross-references GB:X58438; NID:g53181; PID:g53182
                                                                                                                                                                                                                                                                                       ##molecule_type DNA
##residues 1-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     209 RASSGPPRRSAARS-SAASGSRPAASGPAARAPAASSARTSAGEGAARGPGAPRAGW 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               150 RAPGRAGRYPAARPAAASAAASRRHRGPAARSSPAAERPAPPRARAEAAAPRRASSS-GS 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##residues 1-264 ##label FRA
##cross-references GB:M30023; EMBL:M37623; NID:g332561; PID:g332566
## #ength 264 #molecular-weight 25613 #checksum 1957
     262
                                         187
                                                                                                                 131 PGNQQGPPPQG-GPQQRPP-QPGNQQGPPPPPGGPQQRPPQPGGNQGGPP-QGGPHP-PPR 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##molecule_type DNA
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                                                                                                                                             1.88;
Local Similarity 25.28;
les 34; Conservation
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                       PGNQQGPPPQGGPQQRPTQPGNQQGPPQQGG-PQAPPRPGNQQGPPPQGPQGPPRTGNQQ 245
                                                                             AATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPR 261
   RGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPA-EEATSLEGALSGTRHSHPS 320
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proline-rich protein MP4 - mouse
#formal_name Mus musculus #common_name house
22-Nov-1993 #sequence_revision 10-Nov-1995 #t
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Gene sequence of mouse B-type proline-rich protein MP4.
Transcriptional start point and an upstream phylogenetic footprint with ets-like and rel/NFkB-like elements.
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                                                                                                                                                         40;
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Pred. No. 1.21e-02;
                                                                                                                                                                           Score 131; DB 2;
Pred. No. 6.89e-03;
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                                                                                                                                                                                           Length 300;
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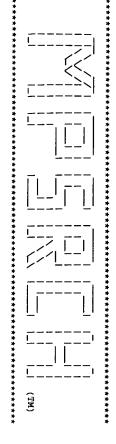
246 -GPPPQGGPQGPPRP 259

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ACCESSIONS
REFERENCE
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Query Match 1.8%;
Best Local Similarity 30.4%;
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#journal
#title
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#journal Mol. Microbiol. (1990) 4:921-932
#title Analysis of three nodD genes in Rhizobium leguminosarum
biovar phaseoli; nodD1 is preceded by nolE, a gene who
product is secreted from the cytoplasm.
#cross-references MUID:91014692
#accession S11790
                                                                                           #introns
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                                                                                                                                                            ##molecule_type DNA
                                                                                                                           ##residues 1-309 ##label LYO
##cross-references EMBL:X07881; NID:g35637; PID:g296669
                                                                                                                                                                                        ##status
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Similarity 31.4%;
38; Conservative
                                                     22/1; 34/1
#superfamily proline-rich protein
#length 309 #molecular-weight 30
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21-Nov-1993 #sequence_revision 13-Jan-1995 #text_change
16-Feb-1997
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                                                                                                                                                                                                                                        Lyons, K.M.; Stein, J.H.; Smithles, O. Genetics (1988) 120:267-278
Length polymorphisms in human proline-rich protein genes generated by intragenic unequal crossing over.
                                                                                                                                                                                                                                                                                                                                                                      $1089 #type complete
proline-rich protein - human
proline-name Homo sapiens #common_name man
07-oct-1994 #sequence_revision 26-May-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nodD3
                                                                                                                                                                                                                                                                                                                                                     08-Sep-1997
                                                                                                                                                                                     preliminary; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1-302 ##label DAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              not compared with conceptual translation
 Score 129; DB 2;
Pred. No. 1.21e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 126; DB 2; Length 302; Pred. No. 2.79e-02; 28; Mismatches 46; Indels
                                                       30936 #checksum 3043
                 Length 309;
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                                                                                                                                                                                                                                                                                                                                                                      #text_change
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311 LSGTRHSHPSVGROHHAGPPSTSRPPRP 338
                                                                                                                                              194 GPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRS
                                                                                                                                                                            122 GPPP-QGGNQSQG-PPPHPGKPEGPPP-QGG-NQSQGPPPRP-GKPE-GPPPQGGNQSQG 175
                                   234 - NKPRGPPPHPGKPQGPPPQEGNKPQRP 260
                                                                       254 LPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSDRG-F-CVVSPARPAE-EATSLEGA 310
                                                                                                         -P-PPRPGKPEGPPPQGGNQSQGPPPRPGKPEGPPPQGGNQSQGPPPRPGKPEGSPSQGG 233
                                                                                                                                                                                                                    45;
                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                    38;
                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                    53;
                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                    12;
                                                                                                                                                                                                                  Gaps
                                                                                                                                              253
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Search completed: Fri Dec 18 18:12:23 1998 Job time: 109 secs.



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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Dec 18 18:12:41 1998; MasPar time 25.51 Seconds 998.601 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: >US-08-951-733-14 (1-949) from US08951733.pep (1 of 2) 7113

1 HASGQRCVLLRTWEALAPAT.....PVEDEALGGTAFVQMPAHGL 949

Searched: PAM 150 Gap 11 74019 seqs, 26840295 residues

Scoring table:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swissprot

Statistics: Mean 54.986; Variance 96.850; scale 0.568

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	

1 3 3 4 4 4 4 4 7 7 7 1 1 1 1 1 1 1 1 1 1 1 1	Result No.
162 153 142 142 133 133 137 125 125 125 125 127 127 127 127 127 127 127 127 127 127	Score
	Query Match I
4 4 3 3 2 7 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Length I
*****************	BG
YHL1_EBV ATIN_HSVBB PRPM_HUMAN PRPL_HUMAN PRPL_HUMAN V70K_TMUSE PRP3_MOUSE PRP3_MOUSE PRP3_MOUSE PRP3_MOUSE NOD1_RHILP MRBA_MOUSE NOD1_RHISN BM8A_MOUSE NOD1_BRAJA PRP1_HUMAN CGEL_XENLA CGEL_XENLA	ID
HYPOTHETICAL BHLF1 PRO ALPHA TRANS-INDUCING P SALIVARY PROLINE-RICH SALIVARY PROLINE-RICH SALIVARY PROLINE-RICH 69 KD PROTEIN PROLINE-RICH PROTEIN M PROLINE-RICH PROTEIN M PROLINE-RICH PROTEIN D BONE MORPHOGENETIC PRO MESSENCHYME FORK HEAD P TESTIS-SPECIFIC PROTEIN D BONE MORPHOGENETIC PRO MESCHATION PROTEIN D BONE MORPHOGENETIC PRO MESCHATION PROTEIN D BONE MORPHOGENETIC PRO MYPOTHETICAL GENE 1 PR TRNA-(MS[2]IO[6]A)-HYD HYPOTHETICAL GENE 1 PR TRNA-MS[2]IO[6]A)-HYD HYPOTHETICAL GENE 1 PR TRNA-MS[2]IO[6]A-HYD HYPO	Description
4.85e-09 4.48e-07 4.48e-07 8.26e-06 4.89e-03 2.95e-03 3.91e-04 2.95e-03 2.9	Pred. No.

RESULT
ID AT
AC P3
DT 01

ATIN_HSVBP STANDARD; P30020; 01-APR-1993 (REL. 25, CREATED)

PRT;

504 AA.

444444333333322224 544444433333322287
111 111 111 1113 1113 1113 1114 1115 1115
498 509 514 633 704 704 705 314 233 328 408 408 408 408 408 408 408 408 408 40
VEZ_HPV08 VEZ_HPV36 VEZ_HPV5B LAIT_YEAST SYN1_RAT SYN1_RAT SYN1_CHITMAN MUC1_HUMAN MUC1_HUMAN TEGU_EBV BAR1_CHITE YFJR_ECOLI YAFY_ECOLI YAFY_MATD_NEUCR CGE3_XENLA MATD_NEUCR YTOK_TYMVC SYN1_BOVIN HISZ_NEUCR ACOL_ECOLI MAPA_RAT
REGULATORY PROTEIN E2. REGULATORY PROTEIN E2. REGULATORY PROTEIN E2. PROLINE-RICH PROTEIN E2. PROLINE-RICH PROTEIN E1. SYNAPSINS IA AND IB. SYNAPSINS IA AND IB. SYNAPSINS IA AND IB. MOUGHN I PRECURSOR (POLLAROR ET EGOMENT PROTEIN BALBIANI RING PROTEIN D. HYPOTHETICAL TRANSCRIP HYPOTHETICAL TRANSCRIP HYPOTHETICAL TRANSCRIP HYPOTHETION PROTEIN D. MATING TYPE PROTEIN D. MATING TYPE PROTEIN ADDING FORK HEAD PRESUNCHYME FORK HEAD PRESUNCHYME FORK HEAD PRESUNCHYME FORK HEAD PROTEIN. SYNAPSINS IA AND IB. PHOSPHORIBOSYL-AMP CYCACONITATE HYDRATASE 1 MICROTUBULE-ASSOCIATED
2.52e-01 1.37e-01 1.37e-01 1.37e-01 1.37e-01 1.37e-01 1.37e-01 1.32e-01

ALIGNMENTS

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•	:::::	Db 365 QDLAAAQRC-PAGPPPTRSGA-AAQRTHR-RPPGCP 397	OY 250 ASRSLPLPKRPRRGAAPEPER-TPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLE	307 TGGRPAAPGAPGTPAAPGPGGGAAVPSGA	OY 194 GPPLYQLGAATQARPPPHASG-PRR-R-LGCERAWNHSVREAGVPLGLPAPGA-	251 GPPPTRSGAAAQ-RTHRRPPGCPRSARNPGCP	Best Local Similarity 30,8%; Fred. NO. 4.85e-09; Matches 48; Conservative 34; Mismatches 60; Indels	h 2.3%; Score 162;	SEQUENCE 6	REPEAT 524 648	REPEAT 399 523	REPEAT 274 398	REPEAT 149 273 1.	DOMAIN 149 648 4 X 125		EMBL; VOISS;	NATURE 310:207	TUFFNELL P.S., BARRELL B.G.;	GIBSON T.J., HATFULL G., HUDSON G.S., SATCHWELL S.C.,	BAER R., BANKIER A.T., BIGGIN M.D., DEININGER P.L.,	SEQUENCE	Ξ	VIRIDAE; DS-DNA ENVELOPED VIRUSES;	HYPOTHETICAL BHLF1	15-JUL-1998 (REL. 36, LAST	DT 21-JUL-1986 (REL. O1, CREATED)	PU3181;	TDS
			ARPAEEATSLE 308	LPPERQEPRLP 364	APGA-RRRGGS 249	PPGAGQRPSGP 306	ls 14; Gaps 12;	560;					,						SEGUIN C.,	FARRELL P.J.,			AHERPESVIRINAE.					

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RESULTION

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Matches 4
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     Matches
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01-MAR-1989 (REL. 10, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
SALIVARY PROLINE-RICH PROTEIN PO (ALLELE M) (CONTAINS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- FUNCTION: RESPONSIBLE FOR TRANSCRIPTIONAL ACTIVATION OF EARLY PROMOTERS (ALPHA GENES) (BY SIMILARITY).
-!- SIMILARITY: TO OTHER HERPESVIRUSES ALPHA TRANS-INDUCING EMBL; Z11610; E264419; -.
PIR; S24229; S24229.
PIR; JC1306; JC1306.
TRANSCRIPTION REGULATION; TRANS-ACTING FACTOR; DNA-BINDING. SEQUENCE 504 AA; 54028 MW; 79F42020 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
ALPHA TRANS-INDUCING PROTEIN (ALPHA-TIE).
BOVINE HERPESVIRUS TYPE 1 (STRAIN P8-2).
VIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRI
                                                                                                                                                                                                     MIM;
                                                                                                                                                                                                                                                                                               PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 89121439.
LYONS K.M., STEIN J.H., SMI
GENETICS 120:255-265(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARPENTER D.E., MISRA V.;
GENE 119:259-263(1992).
                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                               SAITOH E., ISEMURA S., SANADA
J. BIOCHEM. 93:495-502(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE; 89121439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRPM_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE;
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                                                                                                                                                                       REPEAT; PAROTID GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 165-234.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    351 APAEAGGGWRRSGSTRTRGRAARSTTGRLQRPCCGPRRRAKC-CRATP-RQRLR--ARGE 406
  Local Similarity hes 43; Conser
                                                                                                                                                                                                                                                                 x07704; E265547; -.
A03295; PIHUSD.
S03175; S03175.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QHHAGPPSTSRPPRPWDTPCPPVYAET 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GPACGGPSRARGGRRRASPANP-FGGT
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                                                                                                                                                                                                                                                P19999; 1CLG
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Similarity 31.3%;
46; Conservative
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                                                                                                 165
234 /
     Conservative
                                                                                                 AA;
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                           2.1%;
29.3%;
                                                                                                 234
23676
                                                                                                                                                                       SALIVA; MULTIGENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMITHIES
                                                                                                    WW;
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VIRUSES; HERPESVIRIDAE; ALPHAHERPESVIRINAE
Score 150; DB 1;
Pred. No. 4.48e-07;
41; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 153; DB 1; L
Pred. No. 1.47e-07;
33; Mismatches 56;
                                                                                                 PEPTIDE P-D.
; ED2D4ADC C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               489
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                                                                                                    CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TETRAPODA;
  53;
                                                  Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 504;
  Indels 10;
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  Gaps
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Best Local S
Matches 4
                                                     PRP4_HUMAN STANDAGE,
P10163; P02813;
P1-UUL-1986 (REL. 01, CREATED)
13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
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P10162; P02813;

01-MAR-1989 (REL. 10, CREATED)

01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)

01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)

SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) (CONTAINS: PEPTIDE P-D)
  HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X07715; E4806; ALT_SEO.
PIR; A03295; PIHUSD.
PIR; S03176; S03176.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAITOH E., ISEMURA S., SANADA
J. BIOCHEM. 93:495-502(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 89121439.
LYONS K.M., STEIN J.H., SM
GENETICS 120:255-265(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 QGGNQSQG-PPPHPGKPERPPP-QGG-NQSHRPPPPP-GKPER-PPPQGGNQSQG-P-PP 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88
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                                                                                                                                                                                                                                                                                                                                       SHPSVGRQHHAGPPSTSRPPRP
                                                                                                                                                                                                                                                                                                                                                                                       APPAGKPQGPPPPPQGGRPPRP 268
                                                                                                                                                                                                                                                                                                                                                                                                                                               RPRRGAAPEPERTPVGQGSWAHPGRTRGPSDR-GFCVVSPARPAE-EATSLEGALSGTRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HPGKPEGPPPQEGNKSRSARSPPGKPQGPPQQEGNKPQGPPPPGKPQGPPPPGGNPQQPQ 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPK 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGTRHSHPSVGRQHHAGPPSTSRPPRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P19999; 1CLG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 2.0%;
Similarity 28.2%;
40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAROTID GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OF 207-276.
83186122.
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276 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27816 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SALIVA; MULTIGENE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMITHIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 142; DB 1;
Pred. No. 8.26e-06;
                                                                                                                                                                                                                                                                                                                                       338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 52;
                                                                                    (ALLELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 276;
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Best Local S
Matches 4
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Best Local
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EMBL; KO3207; G190508; -.
EMBL; X07882; G296670; -.
HSSP; P19999; 1CLG.
MIM; 168730; -.
MIM; 180990; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LT 6
V70K_TYMV
P10357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                MORCH M.D., BOYER J.C., HAENNI A.L.;
NUCLEIC ACIDS RES. 16:6157-6173(1988).

-!- FUNCTION: NOT KNOWN.
-!- SIMILARITY: TO 65 TO 70 KD PROTEIN FROM OTHER TYMOVIRUSES.
EMBL; X07441; G6223; ALT_SEQ.
PIR; S01955; S01955.
SEQUENCE 628 AA; 69195 MW; 9E64ED49 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 KD PROTEIN.
TURNIP YELLOW MOSAIC VIRUS.
VIRIDAE; SS-RNA NONENVELOPED VIRUSES; TYMOVIRIDAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-1989 (REL. 10,
01-AUG-1992 (REL. 23,
01-AUG-1992 (REL. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT; PAROTID GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAEDA N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EUTHERIA; PRIMATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     155
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                                                                                                                                           157
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    250
                                                 215
                                                                                             194
                                                                                                                                                                                                                                                                                                                                                                                                                                                EQUENCE FROM N.A. EDLINE; 88289359.
                                                                                                                                                                                     Match 1.9%;
Local Similarity 25.0%;
ses 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EDA N., KIM H.-S., AZEN E.A., SMITHIES BIOL. CHEM. 260:11123-11130(1985).
                                                                                                                                         GPVLTETKPRTSVRQPRSATRGPSFRPILLPKV-VH-VHDDPPHSSLRPRGSRSRQLQPT 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRHSHPSVGRQH-HAGPPSTSRPPRP 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QQPQDPPAGKPQGPPPPPQGGRPPRP 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PPHPGKPEGPPPQEGNKSRSARSPPGKPQGPPQQEGNKPQGPPPPGKPQGPPPAGGNP 213
                                            VRRPLLAPNQFHSPRQPPPLSDDPGILGPRPLAPHSTRDPPPRPI-TPGPSN-THDLRPL 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSDR-GFCVVSPARPAEEATSLEGALSG 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSL 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPP-QGGNQSQGTPPPPGK-PERPPP-QGG-NQSHRPPPPP-GKPER-PPPQGGNQSQG- 154
  ASRSLPLPKRPRRGAAPEPERTPVG-QGSWA-HPGRTRGPSDRGFCVVSPARPAEEATSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40;
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247 AA;
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larity 27.4%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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177
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25108
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LAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMITHIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ¥.
                                                                                             -GPR-RRLGCERAWNHSVREAGVPLGLPAPGAR-RR-GGS 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE UP
                                                                                                                                                                                     Score 137; DB 1;
Pred. No. 4.88e-05;
64; Mismatches 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 133; DB 1; Length 247; Pred. No. 1.97e-04; 40; Mismatches 56; Indels
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D -> A (IN REF. 2).
D -> G2BE90B8 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>0</u>
                                                                                                                                                                                          Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ON UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            628
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                                                                                                                                                                                                                                    Length 628;
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Best Local Similarity 27.0%;
                                                                                                                                                                                                                                                                                                             P05143;
P05143;
13-AUG-1987 (REL. 05, L.
13-AUG-1987 (REL. 05, L.
01-OCT-1994 (REL. 30, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                         PRP.
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-AUG-1987 (REL.
13-AUG-1987 (REL.
01-OCT-1994 (REL.
                                            SEQUENCE FROM N.A.
MEDLINE; 86059475.
ANN D.K., CARLSON D.M.;
ANN D.K., CARLSON D.M.;
J. BIOL. CHEM. 260:15863-15872(1985).
EMBL; M12100; G200549; -
HSSP; P19999; 1CLG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANN D.K., CARLSON D.M.;
J. BIOL. CHEM. 260:1863-15872(1985).
EMBL; M12099; G200547; -.
HSSP: P1999; ICLG.
REPEAT; SALIVA; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRP.
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
                            REPEAT;
                                                                                                                                                                                                                              EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRP3_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. WEDLINE; 86059475.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROLINE-RICH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            321 VGRQHHA--GPPSTSRP-PRPWDTPCPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        195 GGPQQQPPQGPPPPGGPQPRPPQGPPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136 PPPPGGPQLRPPQGPPPPAGP-QPRPPQGPPPPAGPQPRPPQGPPTTGPQPRPTQGPPPT 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   421 NHAQC-PYGVLLKTHCPLRA-AVTPAAGVCAREKPQGSVAAPEEEDTDPRRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                203 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76 PPQGPPPPGGPQPRPPQGPPPPGGPQPRPPQGPPPGGPQQRPPQGPPPPGGPQPRPPQG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAPE-PE-RTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPS
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  SALIVA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     261 AA;
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(REL. 30, LAST ANNOTATION
PROTEIN MP-2 PRECURSOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16
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. 05, LAST SEQUENCE ANNIA
                                                                                                                                                                                                                                                                                                                                                       05, CREATED)
05, LAST SEQUENCE UPDATE)
30, LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  261 F
26034 MW;
                                                                                                                                                                                                                                                      CHORDATA;
                                                                                                                                                                                                                                                                                                                                  MP-3 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 125; DB 1;
Pred. No. 2.95e-03
33; Mismatches 6
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PROLINE-RICH PROTEIN MP-2.

9D830DAF CRC32;
                                                                                                                                                                                                                                                      VERTEBRATA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             296 AA
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P34820;
01-FEB-1994
01-FEB-1994
15-JUL-1998
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                                                                                        BMP8_HUMAN
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PROSITE; PS00044; HTH_LYSR_FAMILY; 1.

NODULATION; TRANSCRIPTION REGULATION; DNA-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RHIZOBIUM LEGUMINOSARUM (BIOVAR PHASEOLI).
PLASMID SYM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1991 (REL. 20,
01-NOV-1991 (REL. 20,
01-NOV-1995 (REL. 32,
NODULATION PROTEIN D
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                                                                                                                                                                                    126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .. MICROBIOL. 4:921-932(1990).
FUNCTION: NODD REGULATES THE EXPRESSION OF THE NOD ABCFE GENES WHICH ENCODE OTHER NODULATION PROTEINS. NODD IS ALSO A NEGATIVE REGULATOR OF ITS OWN EXPRESSION. BINDS FLAVONOIDS AS INDUCERS. SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
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                                                                                                                                                                                                                                                                                                                                                                                       LMIERNLTAAARSINLSQPAMSAAVRRL-RSYFRDEL-FIMRGREFVPTP-R-AEDLAPA 72
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                                                                                                                                                                                                                              L 131
                                                                                                                                                                                                                                                                        AFRALVAQCIVCVPWDA-RPPPAAPSFRQVSCLKELVARVL-QRLCERGAKNVLAFGFAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGPQPRPPQGPPPPAGPQPRPPQGPPPP
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                                                                                                                                                                                                                                                                                                                    IREALQHIRLNIIPWDKFTPDQSDRHFR-VS-LCDFVTVVLFQKILERLAREAPGISFDL 130
                                                                                                                                                                                                                                                                                                                                                             LLRTWEALAPATP-AMPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             302 AA;
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                    (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.8%;
larity 31.4%;
Conservative
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llarity 26.4%;
Conservative
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                                                                                            STANDARD;
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  28,
36,
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34274 MW;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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LAST ANNOTATION UPDATE)
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Pred. No. 3
38; Mismat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 126; DB 1;
Pred. No. 2.12e-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H-T-H MOTIF (BY SIMILARITY).; ED62D2FA CRC32;
                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                          402 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 302
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Best Local
                                                              SEQUENCE FROM N.A.

MEDLINE; 97312712.

MUDRA N., IIDA K., KAKINUMA H., YANG X.-L., S
GENOMICS 41:489-492(1997).

-I- FUNCTION: MIGHT BE INVOLVED IN THE FORMAT

MESERCHYMAL TISSUES (BY SIMILARITY).

-I- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).

-I- SIMILARITY: CONTAINS 1 FORK-HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                              MFH1_HUMAN STANDARD; PRT; 501 AA.
Q99958;
15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
MESENCHYME FORK HEAD PROTEIN 1 (MFH-1 PROTEIN)
                                                                                                                                                                                                                                                                                              SIGNAL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M97016; G189390; PIR; A45056; A45056. HSSP; P08112; 1TFG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OEZKAYNAK E., SCHNEGELSBERG P.N.J., JIN D.F., CLIFFORD G.M.,
WARREN F.D., DRIER E.A., OPPERMANN H.;
J. BIOL. CHEM. 267:25220-25227 (1992).

-i- FUNCTION: INDUCES CARPILAGE AND BONE FORMATION. MAY BE THE
OSTEOINDUCTIVE FACTOR RESPONSIBLE FOR THE PHENOMENON OF
EPITHELIAL OSTEOGENESIS. PLAYS A ROLE IN CALCIUM REGULATION
AND BONE HOMEOSTASIS (BY SIMILARITY).
                            EMBL; Y08223
MIM; 602402;
                                                                                                                                                                                                                                                                                                                                                     FKH-14).
FKHL14 OR MFH1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HOMO SAPIENS (HUMAN)
EUKARYOTA; METAZOA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                     EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBUNIT: HOMODIMER, DISULF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BONE MORPHOGENETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 93094231.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           253 SLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 194 GPPLYQLGAATQA-RPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 GLALCALGGGGPGLRPPP-GC-PQRRLG-ARERRDVQREILAVLGLPGR-PRPRAPPAAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 RLP 70
                                             Y08223; E303016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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  PS00657; FORK_HEAD_1;
                                                                                                                                                                                                                                                                                     PRIMATES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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TO THE TGF-BETA FAMILY
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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Pred. No. 2.95e-03;
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POTENTIAL.
                                                                                                                                                                                                                                                                                                        VERTEBRATA;
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                                                                                                                                               IN THE FORMATION
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                                                                                                                                                                                                                                                                                                        TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TETRAPODA;
                                                                                                                                                                                          SUGIYAMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 402
                                                                                                                                                                                                                                                                                                                                                                                                   (TRANSCRIPTION FACTOR
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Best Local
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Best Local
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                                                                                                                                                                Matches
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Q01755;
Q1-NOV-1995
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDAT
TESTIS-SPECIFIC PROTEIN PBS13.
                                                                                                                                                                                                                                                                                   REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAZARAKIS N.D., NELKI D., LYON M.F., EVANS FREEMONT P., DUDLEY K.;
DEVELOPMENT 111:561-571(1991).
-1- FUNCTION: POSSIBLY PLAYS AN IMPORTANT AND FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MUS MUSCULUS (MOUSE).
EURARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSCRIPTION DNA_BIND
                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X52128; G54853; -. PIR; S22933; S22933. MGD; MGI:98544; TCP11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -
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MEDLINE; 91372153
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                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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                                       94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPERMATOCYTE STAGE.
SIMILARITY: SOME TO YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE SPECIFICITY: TESTIS.

DEVELOPMENTAL STAGE: FIRSTLY EXPRESSED
                                                                                                  SARGTDRVGSTVARARPPSPQGPRRGAVKTAPRGPVGHGGLRTGPTSRCPQPSARAKLPS 93
                               VTRGAPLPPSPG-KGHLGGTPSSH 116
                                                                               PAPGARRRGGSASRSLPL-PKRPRRGAAPEPERTPVGQGS-WAHP-GRTRGPSDRG-FCV 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YSSGDKEQLRPSFLLSSLRPSLTGARRLVETIFLG 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NHSGDLNHL-PGHTFAAQQQTFPNVREMFNSHRLG 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPARPAEEATSLEGALSGTRHSHPSVGRQH-HAGPPSTSRPPRPWDTPCPPVYAETKHFL 354
  VSPARPAEEATSLEGALSGTRHSH
                                                                                                                                                                                                                                                                               ; SPERMATOGENESIS; I
206
276
318
419
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311
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Similarity 28.4%;
27; Conservat'
                                                                                                                                                                                   1.8%;
Similarity 35.7%;
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163
387
397
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501 i
                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FORK_HEAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FORK_HEAD_2; 1.
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                                                                                                                                                                                                                                                61970 MW;
                                                                                                                                                                                                                                         S; REPEAT; COILED COIL.
COILED COIL (8 HEPTADS).
COILED COIL (8 HEPTADS).
COILED COIL (2 HEPTADS).
COILED COIL (10 HEPTADS).
COILED COIL (10 HEPTADS).
LEUCINE-RICH REPEATS.
LER 1.
LRR 3.
LRR 3.
LRR 3.
LRR 3.
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                                                                                                                                                            Score 127;
Pred. No. 1.
19; Mismatc
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Pred. No. 2.95e-03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FORK-HEAD.
POLY-ARG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALA/PRO-RICH.
POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIS-RICH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EVANS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEAR PROTEIN.
                                                                                                                                                                                   DB 1;
L.51e-03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E.P., RUDDY
                                                                                                                                                                30;
                                                                                                                                                                                                      Length 566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ΙN
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BM8A_MOUSE
P34821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE000065; G2182301; -.

PROSITE; PS00044; HTH_LYSR_FAMILY; 1.

RODULATION; TRANSCRIPTION REGULATION; DNA-BINDING; ACTIVA REPRESSOR; MULTIGENE FAMILY; PLASMID.

DNA_BIND 23 42 H-T-H MOTIF (BY SIMILARITY).

SEQUENCE 322 AA; 36460 MW; FA5238EE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOD1_RHISN P55359;
                                                                             MEDLINE; 93094231.

OEZKAYNAK E., SCHNEGELSBERG P.N.J., JIN D.F., CLIFFORD G.M.,
WARREN F.D., DRIER E.A., OPPERMANN H.;
U. BICOL. CHEM. 267:25220-25227(1992),
J. BICOL. CHEM. 267:25220-25227(1992),
-i- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION. MAY BE THE
OSTEOINDUCTIVE FACTOR RESPONSIBLE FOR THE PHENOMENON OF
EPITHELIAL OSTEOGENESIS. PLAYS A ROLE IN CALCIUM REGULATION
AND BONE HOMOGIASIS (BY SIMILARITY).
-i- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
-i- DEVELOPMENTAL STAGE: EXTENSIVE EXPRESSION FOUND IN 8-DAY EMBRYOS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQ
01-CCT-1996 (REL. 34, LAST ANN
BONE MORPHOGENETIC PROTEIN 8A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE; 97305956. FREIBERG C.A., FELLAY R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RHIZOBIUM SP. (STRAIN NGR234).
PLASMID SYM PNGR234A.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (REL. 35, C. 01-NOV-1997 (REL. 35, L. 01-NOV-1997 (REL. 35, L. NODULATION PROTEIN D I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BMP8A OR BMP8 OR BMP-8.
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NODD1 OR Y4AL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -11 FUNCTION: NODD REGULATES THE EXPRESSION OF THE NOD ABCFE GENES WHICH ENCODE OTHER NODULATION PROFEINS. NODD IS ALSO A NEGATIVE REGULATOR OF ITS OWN EXPRESSION. BINDS FLAVONOIDS AS INDUCERS.
-1- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NATURE 387:394-401(1997)
                                                                                                                                                                                                                                                                                                                                                                             TISSUE-EMBRYO
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RHIZOBIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 -II-LSDFMTLMFLERVVVRVAREAPAVSFELL
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                                                        FELL
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28; Conser
                                                     DRASTICALLY IN 10-DAY EMBRYOS AND VIRTUALLY ABSENT IN
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larity 30.1%;
Conservative
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BELONGS
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35, LAST SEQUENCE UPDATE)
35, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHORDATA;
TO THE TGF-BETA FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BAIROCH A., BROUGHTON W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE UPDATE)
ANNOTATION UPDATE)
8A PRECURSOR (BMP-8A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 121; DB 1; L
pred. No. 1.09e-02;
23; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (OSTEOGENIC PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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Best Local S
Matches 2
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Best Local Similarity 38.7%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDILINE; 90269039.

CHEE M.S., BANKIER A.T., BECK S., BOHNI R., BROWN C.M., CERNY R.,
HORSNELL T., HUTCHISON C.A. III, KOUZARIDES T., MARTICNETTI J.A.,
PREDDIE E., SATCHWELL S.C., TOMLINSON P., WESTON K.M., BARRELL B.G.;
CURR. TOP. MICROBIOL. IMMUNOL. 154:125-169(1990).

EMBL; X17403; E27260; -.

EMBL; X17403; E27260; -.

PIR; SO9824; S09824.

HYPOTHETICAL PROTEIN.

SEQUENCE 431 AA; 44309 MW; 232AB9D7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UL61_HCMVA
P16818;
01-AUG-1990 (
01-AUG-1990 (
01-FEB-1991 (
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DISULFID
DISULFID
DISULFID
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HUMAN CYTOMEGALOVIRUS (STRAIN AD169).
VIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE; BETAHERPESVIRINAE.
[1]
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CHAIN
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325 TAPDGAPGRWDGPADGPAPGLGRG 348
:| | | | | : :|: ||
270 RTPVG-QGSWAHPGRTRGPS-DRG 291
                                                                                                   211
                                                                                                                          194 GPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRS 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    254 LP 255
                                                                                                                                                                                            y Match 1.7%;
Local Similarity 32.1%;
hes 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 QP 69
                                                                                                HASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSAS-RSLPLPKRPRRGAAPEPE 269
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261
298
327
331
363
155
340
AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (REL. 15, CREATED)
(REL. 15, LAST SEQUENCE UPDATE)
(REL. 17, LAST ANNOTATION UPDATE)
L PROTEIN UL61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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399
396
398
398
155
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                                                                                                                                                                                            Score 118; DB 1; Length 431 Pred. No. 2.87e-02; 20; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
BONE MORPHOGENETIC P
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 118; DB 1; Le
Pred. No. 2.87e-02;
12; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7075A1ED CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     431 AA.
                                                                                                                                                                                                                                               Length 431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 399;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.
                                                                                                                                                                                               Gaps
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Search completed: Fri Dec 18 18:14:00 1998
Job time: 79 secs.

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* * * *	(ME)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Dec 18 18:37:59 1998; MasPar time 18.72 Seconds 800.790 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: >US-08-951-733-14 (640-940) from US08951733.pep (2 of 2) 2214

Sequence: 1 TSRLRFIPKPDGLRPIVNMD.....NLRKTVVNFPVEDEALGGTA 301

Scoring table: PAM 150 Gap 11

Searched: 165420 segs, 49795644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb16
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 47.179; Variance 86.093; scale 0.548

SUMMARIES

22 21 23 33 34 44 35 45 45 45 45 45 45 45 45 45 45 45 45 45	Result
2214 2214 1596 375 375 375 201 108 108 108 109 109 99 99 99 99 99	Score
1000 1000 1000 1000 1000 1000 1000 100	Query Match
1132 1132 1122 1122 1122 1122 1988 988 989 1031 1002 1002 516 13410 1341	Length [
444660000000000000000000000000000000000	DB 1
014746 014783 070372 07037338 0013338 006163 006163 0051242 0051293 0065183 0065183 0065181 0065181 0066581 0066581 0066581 0066581 0066581 0066581 0066581 0066581 0066581 0066581 0066581 0066581 0066581 0066581 0066581	ID
TELOMERASE REVERSE TRA TELOMERASE CATALYTIC S STELOMERASE REVERSE TRA TELOMERASE SUBUNIT P12 CHROMOSOME XII COSMID HYPOTHETICAL 10.7 KD p GTP-BINDING PROTEIN (NAD HYPOTHET REDUCTASE (NAD FLAVONOID 3',5'-HYDROX POLYPROTEIN PRECURSOR. POLYPROTEIN PRECURSOR. POLYPROTEIN PRECURSOR. YAFJ. HYPOTHETICAL PROTEIN M ORF (FERGMENT). MATURASE-RELATED PROTE NEUROFILAMENT-LIKE PRO HYPOTHETICAL 66.2 KD P	Description
0.00e+00 0.00e+00 0.00e+00 0.00e+00 3.34e-52 3.34e-52 1.81e-17 4.10e-08 6.37e-02 6.37e-02 5.85e-01 1.08e+00 1.08e+00 1.08e+00 1.08e+00 1.08e+00 1.08e+00 1.08e+00 1.08e+00 1.08e+00 1.08e+00 1.08e+00	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	ដ	30	29	28	27	26	25	24	23	22	21
94	93	93	93	93	94	94	95	95	95	96	96	96	96	95	95	96	96	95	96	96	97	97	97	99
4.2	4.2	4.2	4.2	4.2	4.2	4.2	4 3	4 .ω	4.3	ω	4.3	4.3	4.3	4.3	4 3	4. 3	4.3	4 ۵	4.3	٠. ۵	4.4	4.4	4.4	4 .5
2910	802	581	528	368	364	314	3411	3410	3410	1216	786	899	625	575	363	363	308	307	286	245	1398	358	275	1176
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026008	P93042	051662	Q41592	067880	012975	001873	Q98803	Q89278	Q89277	Q62884	Q34832	Q94607	044733	036013	057518	Q69275	P96605	033708	039304	059069	P72186	065581	045575	Q08236
RNA POLYMERASE I.	ROOT HAIR DEFECTIVE 3.	THREONYL-TRNA SYNTHETA	WPK4 PROTEIN KINASE.	GLUCOSYL TRANSFERASE I	ALDOLASE.	SIMILAR TO CUTICULAR C	POLYPROTEIN.	POLYPROTEIN.	POLYPROTEIN.	VASCULAR PROTEIN TYROS	INTRON ORF.	JUVENILE HORMONE BINDI	F54D7.1 PROTEIN.	HYPOTHETICAL PROTEIN C	FRUCTOSE-1,6-BISPHOSPH	PROTEIN KINASE; GLYCOP	PROBABLE TRANSPORT ATP	THYMIDINE DIPHOSPHO-4-	NO COUNTERPARTS IN HSV	245AA LONG HYPOTHETICA	PYROLYSIN.	FRUCTOSE-BISPHOSPHATE	F56A8.4.	CHROMOSOME XV READING
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Matches 30
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                                                                                                                                        070372;
01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
TELOMERASE REVERSE TRANSCRIPTASE.
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEYERSON M., COUNTER C.M., EATON E.N.,
CADDLE S.D., ZIAUGRA L., BEIJERSBERGEN
BACCHETTI S., HABER D.A., WEINBERG R.A.
CELL 90:785-795(1997).
EMBL; AF018167; G2347129; ...
SEQUENCE 1132 AA; 126937 MW; C1E5E2
                   GREENBERG R.A., ALLSOPP R.C., ONCOGENE 0:0-0(1998).
EMBL; AF051911; G3005592; -.
                                                                                                                                                                                                                                                                                                                                      070372
                                                                                           SEQUENCE FROM N.A.
  RNA-DIRECTED
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EUKARYOTA; METAZOA; CHORDATA;
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R.L., DAVIDOFF
                                                                          MORIN
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                                                                          R.A.;
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O13339;
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JT 01-JAN-1998 (TREMBLREL 07, LAST SEC

DT 01-AUG-1998 (TREMBLREL 07, LAST AN)

TTTOMERASE REVERSE TRANSCRIPTASE 1.
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PFAM; PF00078; rvt.
RNA-DIRECTED DNA POLYMERASE.
RNA-DIRECTED BNA POLYMERASE.
                                                                                                                                                                                                                                                                                                                                                                                                     LYNE M., RAJANDREAM M.A., BARRELL B.G., VOLCKAERT G.; SUBMITTED (MAR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS. EMBL; AFO15783; G2340168; -.
EMBL; AL022299; E1285360; -.
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NAKAMURA T.M., MORIN G.B.,
LINGNER J., HARLEY C.B., C.
SCIENCE 277:955-959(1997).
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05, LAST SEQUENCE UPDATE;
07, LAST ANNOTATION UPDATE;
vscriptase 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAPMAN
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V
                                                                                                                                                                                                                                               Score 375; DB 3; L. Pred. No. 3.34e-52; 51; Mismatches 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred.
68; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                         39C385A7 CRC32
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RESULT OCCUPANT OCCUP
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                                                                         Query Match
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O00939;
01-JUL-1997 (TREMBLREL. 04, CREATED)
01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
TELOMERASE SUBUNIT P123.
EUPLOTES AEDICULATUS.
EUPLOTES AMTTOCHONDRIAL EUKARYOTES; ALVEOLATA; CI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O13338 PRELIMINARY; PRT; 989 AA.
O13338; O1-JAN-1998 (TREMBLREL. 05, CREATED)
O1-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
O1-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEMBL; ARVILLE PERBL; ARVILLE PERBL; PEODOT8; TVE.
RNA-DIRECTED DNA POLYMERASE.
989 AA; 116456 MW;
                                                                                                                                           SCIENCE 276:561-567(1997).
EMBL; U95964; G2072336; -.
SEQUENCE 1031 AA; 122562 MW;
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE; 97274210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAKAMURA T.M., MORIN G.B., CHAPMAN LINGNER J., HARLEY C.B., CECH T.R.; SCIENCE 277:955-959(1997).
EMBL; AF015783; G2340169; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRT1.
SCHIZOSACCHAROMYCES
                                                                                                                                                                                                                                                                                             LINGNER J., HUGHES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  761
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Local Similarity 30.7%;
hes 65; Conservative
                                  Local
                                                                                                                                                                                                                                                               T. R.
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   Similarity 77; Conser
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       Conservative
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ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                             T.R.,
                                      9.18;
                                                                                                                                                                                                                                                                                             SHEVCHENKO A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 375; DB 3;
Pred. No. 3.34e-52;
51; Mismatches 90
Score 201; DB 5;
Pred. No. 1.81e-17;
82; Mismatches 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FDE74202 CRC32;
   Mismatches 126;
                                                                                                                                                  21A885CD CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALVEOLATA; CILIOPHORA;
                                                                                                                                                                                                                                                                                             MANN M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90;
                                                                 Length 1031;
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   Indels
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   Gaps
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C. STRAIN-S288C (AB972);

RX MEDLINE; 97313267.

RX MEDLINE; 97313267.

RX A JOHNSTON M., HILLIER L., RILES L., ALBERMANN K., ANDRE B., ANSORGE W.,

RA JOHNSTON M., HILLIER L., DUBOIS E., DUSTERHOFT A.,

RA LEWIS V., BRUCKNER M., DELIUS H., DUBOIS E., DUSTERHOFT A.,

RA HEUSS-NEITZEL D., HILBERT H., HILGER F., KLEINE K., KOTTER P.,

RA LOUIS E.J., MESSENGUY F., MEWES H.W., MIOSGA T., MOSTL D.,

RA LOUIS E.J., MESSENGUY F., MEWES H.W., MIOSGA T., MOSTL D.,

RA LOUIS E.J., MESSENGUY F., MEWES H.W., MIOSGA T., MOSTL D.,

RA MULLER-AUER S., NENTWICH U., OBERMAIER B., PIRAVANDI E., POHL T.M.,

RA MULLER-AUER S., DURNEILLE B., SCHWARER C., SCHWARZ S.,

RA MULLER M., SCHERENS B., SCHOLLER P., SCHWAGER C., SCHWARZ S.,

RA UNDERWOOD A.P., URRESTARAZU L.A., VANDENBOL M., VERHASSELT P.,

VERTENDERE H. STATEBANN E., SCHWALER E.,

VENTER H. VENTER A., WEDLER E.,

VENTER B., SCHERER E.,

VENTER B., SCHERER E.,

VENTER B., VORT M., VOLUKAER E.,

VENTER B., VENTER B., WEDLER E.,

VENTER B., VENTER B., WEDLER E.,

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Q06163;
                                                                                                                                      SUBMITTED (JUL-1997) TO EMBL; U20618; G662136; - SEQUENCE 884 AA; 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TREMBLREL 01, 01-NOV-1996 (TREMBLREL 01, 01-AUG-1998 (TREMBLREL 07, CHROMOSOME XII COSMID 8543.
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-S288C (AB972); WATERSTON R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B
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EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                 CHERRY
                                                                                                                                                                                                                                                                      STRAIN=S288C (AB972);
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=S288C (AB972);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                    SUBMITTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBMITTED (MAR-1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   915
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       Local Similarity nes 68; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGFKFNMKKLQTSFPL 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVI-AS-II 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FGFAVENYDDVMKKYEEFVCK-WKQVGQPKLFFATMDIEKCYDSVNREKLSTFLKTTKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GKLRLIPKKTTFRPI--MTF--NKKIVNSDRKTTKLTTNTKLLNSHLMLKTLKNRMFKDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EYGCVVNLRKTVVNFPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHA-VRIRGKSYVQCQGIPQGSILSTLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DLNAKKTLIVEAKORNYFKKDNLLQPVIN-ICQYNYINFNGKFYKQTKGIPQGLCVSSIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KPQ---NTYCV--RRYAVV-Q-KAAHGHVRKA-FKSHVSTLT-DLQPYMRQF-V-AHLQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKALFS--VLNYERARR-PGL
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                                                                                                                                                                                                                                          J.M.;
                                                                                                                                                                                                                                                                                                                                                                                (FEB-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIMMERMANN F.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
       Conservative
                                       6.7%;
                                                                                                                                             102662 MW;
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                                                                                                                                                                                                          EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                    EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL/GENBANK/DDBJ
Score 148;
Pred. No. 4.
67; Mismato
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LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZOLLNER A.,
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                                                                                                                                             1A94320F CRC32
          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            884
       4.10e-08;
atches 93;
                                                                      DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HANI J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B
                                                                                                                                                                                                                                                                                                                                                                                    DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DATA BANKS
                                                                   Length 884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HOHEISEL J.D.;
       Indels
          32;
       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      914
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RESULT 8
ID 051242
AC 051242;
DT 01-JUN-1998
DT 01-JUN-1998
DT 01-AUG-1998
DE HYPOTHETICAL
GN BB0224
OS BORRELIA BURG
OC SPIROCHAETACI
CO SPIROCHAETACI
RN [1]
RP SEQUENCE FROM
RC STRAIN-4TCC:
RN [1]
RA DUGHERRY BA
EFRASER C.M.,
RA LATHIGRA R.,
RA LATHIGRA R.,
RA DUGHERRY BA
RA LATHIGRA R.,
RA DUGHERRY BA
RA VAN VUGT R.,
RA UTTERBACK T.,
RA UTTE
RESULT
AC O2
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DT 02
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(C STRAIN-ATCC 35210 / B31;

(C STRAIN-ATCC 35210 / B31;

(X MEDLLINE; 98065943.

(X FRASER C.M., CASJENS S., HUANG W.M., SUTTON G.G., CLAYTON R.A.,

(A FRASER C.M., CASJENS S., HUANG W.M., DODSON R., HICKEY E.K., GWINN M.,

(A LATHIGRA R., WHITE O., KETCHUM K.A., DODSON R., HICKEY E.K., GWINN M.A.

(A DOUGHERTY B., TOMB J.-F., FLEISCHAANN R.D., RALZBERG S., HANSON M.,

(A DOUGHERTY B., TOMB J.-F., FLEISCHAANN J.,

(A VAN VUGT R., PALMER N., ADAMS M.D., GOCAYNE J.D., WEIDMAN J.,

(A VAN VUGT R., PALMER N., ADAMS M.D., GOCAYNE J.D., WEIDMAN C.,

(A UTTERBACK T., WATTHEY L., MCDONALD L., ARTIACH P., BOMMAN C.,

(A UTTERBACK T., WATTHEY L., MCDONALD L., ARTIACH P., BOMMAN C.,

(A SMITH H.O., VENTER J.C.;

(A SMITH H.O., VENTER J.C.;

(A SMITH H.O., VENTER J.C.;

(A SMITH B.O.) 580-586(1997).

(B SEQUENCE 94 AA; 10659 MW; 5C04D3BA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 4.9%;
Best Local Similarity 26.8%;
                                                                                         025293;
025293;
01-JAN-1998
01-JAN-1998
01-JUN-1998
01-BINDING
   HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI). PROKARYOTA; GRACILICUTES; SCOTOBACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE).
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; SPIROCHETES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPIROCHAETACEAE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LFLSFSIIISCRVKGIVIKNGNCIKAKGISEKEILLASVSCNLHYDLNSDSINDGIKANN 71
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                                                                                                                                                                                                                                                                                                                                                                               LLLRLVDDFLL 894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LFDVF-LRFMCH-HAVRIRGKSYVQCQGIPQGSIL-STLLCSLCYGDMENKLFAGIRRDG 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CVVNLRKTV-VNFPVEDEAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NVR-TVHLSNQDVIN----VV-E----M-EIF-K-T---ALWVEDKCYIREDGLFQGSSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PQ-DRLTEVIASIIKPQNTYCVR-RYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVA 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRMECMR-ILKDALKNENGFFVRSQY-FFNINT-G-VLKLFNV-VNASRVPKPY-ELYID 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VLNYERARRPGLLGASVLGLDDI-HRAWRTFVLRV-RA-QDPPPELYFVKVDVTGAYDTI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLLCSLCYGDM-E-NKLF-AGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19;
                                                                                         3 (TREMBLREL. 05, 03) (TREMBLREL. 05, 13) (TREMBLREL. 06, 14) FROTEIN (GTP1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TREMBLREL. 06, CREATED)
(TREMBLREL. 06, LAST SEQUENCE UPDATE)
(TREMBLREL. 07, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                      CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 108; DB 2;
Pred. No. 6.37e-02;
19; Mismatches 30
                                                                                                                                                                                                                                                      366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPIROCHAETALES;
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Best Local (
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Best Local (
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01-JUN-1998
01-JUN-1998
01-AUG-1998
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CAENORHABDITIS ELEGANS.
CAENORHABDITIS ELEGANS.
ACOELOMATES; NEMATODA;
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045321
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NATURE 388:539-547(1997).
NEONO571; G2313689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., BONFIELD BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A., CRAXTON M. DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L., GARDNER A., GREEN HAWKINS T., HILLIER L., JIER M., JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P., LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M., PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R., SMALDON N., SMITH SONNHAMMER E., STADEN R., SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERNTON R., WATSON A., WEINSTOCK L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 97394467.

TOMB J.-F., WHITE O., KERLAVAGE A.R., CLAYTON R.A., SUTTON G.G., TOMB J.-F., WHITE O., KETCHUM K.A., KLENK H.-P., GILL S., DOUGHERTY ELEISCHMANN R.D., KETCHUM K.A., KLENK H.-P., GILL S., DOUGHERTY NELSON K., QUACKENBUSH J., ZHOU L., KIRKNESS E.F., PETERSON S., LOFTUS B., RICHARDSON D., DODSON R., KHALAK H.G., GLODEK A., MCKENNEY K., FITGGERALD L.M., LEE N., ADAMS M.D., HICKEY E.K., MCKENNEY K., GOCAYNE J.D., UTTERBACK T.R., PETERSON J.D., KELLEY COTTON M.D., WEIDMAN J.M., FUJII C., BOWMAN C., WATTHEY L., WALLEY WALLEY WAS ALLEY WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WILKINSON-SPROAT J., WOHLDMAN P.;
NATURE 368:32-38(1994).
EMBL; Z96047; E1246680; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBMITTED
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757 PQ 758
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                                                                                                                                                                                                                                                                                                                         Match 4.7%;
Local Similarity 26.4%;
    83
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Local Similarity 25.8%;
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    SILSSRNIFELR 94
                                                                                      RRYAVVQKAAH-GHVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLNE
                                                                                                                                                                                  HWNTIIRKSAHLSLYRNIFKKKRRQKLNYR-HMSTFLASSENISNIRDTVVLLEINKLSQ
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                                                                                                                                                                                                                                                                                            19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (JAN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS
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GIREMBLREL.
GIREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          561 AA;
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                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65807 MW;
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07,
                                                                                                                                                                                                                                                                              Score 104; DB 5; L
Pred. No. 2.29e-01;
25; Mismatches 25;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 6.37e-02;
21; Mismatches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1C710A97 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          869A60B1 CRC32;
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., DOUGHERTY B.A.,
                                                                                                                                                                                                                                                                                        ų.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BONFIELD J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ψ
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Q1-FEB-1997 (TREMBLREL 02, C
Q1-FEB-1997 (TREMBLREL 02, L
Q1-JUN-1998 (TREMBLREL 06, L
FLAVONOID 3',5'-HYDROXYLASE (
GENTIANA TRIFLORA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              066583
066583;
01-AUG-1998
01-AUG-1998
01-AUG-1998
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                                                                                                          PROSITE: PSO0086; CYTOCHROME_P450; 1.
FFAM; PF00067; P450.
OXIDOREDUCTASE; MONOOXYGENASE; ELECTRON TRANSPORT; MEMBRANE;
BINDING 453 453
HEME (BY SIMILARITY).
SEQUENCE 516 AA; 58088 MW; F68F55B9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                        T 12
Q96581
                                                                                                                                                                     TANAKA Y., YONEKURA K., FUKUCHI-MIZUTANI M., ASHIKARI T., KUSUMI T., PLANT CELL PHYSIOL. 37:711-716(1996).
-!- SIMILARITY: BELONGS TO THE CYTOCHROME P4'
EMBL, D85184; G1620009; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJJ FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.; NATURE 392:353-358(1998).
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01-AUG-1998 (TREMBLREL. 07,
01-AUG-1998 (TREMBLREL. 07,
01-RITRITE REDUCTASE (NAD(P)H)
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EUKARYOTA; PLANTAE; EMBRYOBIONTA; MAGNOLIOPHYTA; MAGNOLIOPSIDA;
ASTERIDAE; GENTIANALES; .
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Local Similarity 32.58;
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 76
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                     MYLKVGSHGLAIASTPDAAKAFLKTL 101
                                                                4.6%;
Similarity 27.9%;
24; Conservation
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                                                                  Score 102; I
Pred. No. 4.2
26; Mismatch
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LARGE SUBUNIT (NAD(P)H).
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d. No. 2.29e-01;
Mismatches 9
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1.29e-01;
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089276;
01-NOV-1996
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Q89275;
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01-NOV-1996 (TREMBLREL.
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            SUBMITTED (NOV
EMBL; U17066;
                                                                                                                                                STRAIN-VACCINE STRAIN 17DD;
DOS SANTOS C.N., POST P.R.,
                                                                                                                                                                                                                                      YELLOW FEVER VIRUS.
VIRIDAE; SS-RNA ENVELOPED
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DOS SANTOS C.N., F
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                                                GALLER R.;
                                                              STRAIN-VACCINE STRAIN 17DD;
                                                                                  SEQUENCE FROM
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                                                                                                                    RES.
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Similarity 32.3%;
21; Conservative
              (NOV-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
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[ P.R., CAI
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LAST SEQUENCE UPDATE)
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Pred. No. 5.85e-01;
14; Mismatches 27;
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Best Local Similarity 32.3%;
Matches 21; Conservative
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STRAIN-MS11;
BARTEN R., MEYER T.F.;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AJ002783; E1198593; -.
SEQUENCE 280 AA; 31556 MW; 34FFDA18 CRC32;
                                                                                                                                                                                                                                                                              LT 15

O50469 PRELIMINARY; PRT; 280 AA.

O50469;
O1-JUN-1998 (TREMBLREL. 06, CREATED)
O1-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
O1-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
YAFJ.
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PROKARYOTA; GRACILICUT
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885 LLRLV 889
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1187 1353 POTENTIAL.
1483 2105 NS3.
2107 2393 POTENTIAL.
2506 2506 NS5.
3410 AA; 379301 MW; 06C3D225 CRC32;
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Pred. No. 5.85e-01;
14; Mismatches 27; Indels 3;
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Tabular output not generated.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Fri Dec 18 18:50:42 1998; MasPar time 22.83 Seconds 672.605 Million cell updates/sec

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Database:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the acore of the result being printed, and is derived by analysis of the total score distribution.

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Mean 3.259; Variance 0.721; scale 4.521

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915 5 0.5 593 16 R93278 Human kidney PTM/PTM (.21e-0) 916 5 0.5 611 7 R88651 Paeudomonas exotoxin (.22e-0) 917 5 0.5 613 8 R40117 Paeudomonas exotoxin (.22e-0) 918 5 0.5 613 6 R40117 Paeudomonas exotoxin (.22e-0) 919 5 0.5 614 6 R39650 Pibriogen binding su (.22e-0) 920 5 0.5 615 6 R39650 Pibriogen binding su (.22e-0) 921 5 0.5 665 16 R89656 Pibriogen binding su (.22e-0) 922 5 0.5 665 17 R86559 Rat NDF encoded by cl. (.22e-0) 923 5 0.5 665 18 R89650 Pibriogen binding su (.22e-0) 924 5 0.5 665 7 R34605 Paeudomonas exotoxin (.22e-0) 925 6 665 17 R86559 Paeudomonas exotoxin (.22e-0) 926 6 6 7 R34605 Paeudomonas exotoxin (.22e-0) 927 5 0.5 665 7 R34605 Paeudomonas exotoxin (.22e-0) 928 5 0.5 665 7 R34605 Paeudomonas exotoxin (.22e-0) 929 5 0.5 668 8 R39550 Paeudomonas exotoxin (.22e-0) 920 5 0.5 668 8 R39550 Paeudomonas exotoxin (.22e-0) 921 5 0.5 669 8 R39550 Paeudomonas exotoxin (.22e-0) 922 5 0.5 669 8 R39550 Paeudomonas exotoxin (.22e-0) 923 6 6 6 7 R34605 Paeudomonas exotoxin (.22e-0) 924 6 8 R39550 Paeudomonas exotoxin (.22e-0) 925 6 6 7 R34605 Paeudomonas exotoxin (.22e-0) 926 7 R34605 Paeudomonas exotoxin (.22e-0) 927 7 R34605 Paeudomonas exotoxin (.22e-0) 928 7 R34605 Paeudomonas exotoxin (.22e-0) 929 7 R34605 Paeudomonas exotoxin (.22e-0) 920 8 R3560 Paeudomonas exotoxin (.22e-0) 921 8 R3560 Paeudomonas exotoxin (.22e-0) 922 8 R3560 Paeudomonas exotoxin (.22e-0) 923 8 R3560 Paeudomonas exotoxin (.22e-0) 924 8 R3560 Paeudomonas exotoxin (.22e-0) 925 8 R3460 Paeudomonas exotoxin (.22e-0) 926 8 R3560 Paeudomonas exotoxin (.22e-0) 927 8 R3560 Paeudomonas exotoxin (.22e-0) 928 8 R3560 Paeudomonas exotoxin (.22e-0) 928 8 R3560 Paeudomonas exotoxin (.22e-0) 929 8 R3560 Paeudomonas exotoxin (.22e-0) 920 8 R3560 Paeudomonas exotoxin (.22e-0) 921 8 R3560 Paeudomonas exotoxin (.22e-0) 922 8 R3560 Paeudomonas exotoxin (.22e-0) 923 8 R3560 Paeudomonas exotoxin (.22e-0) 924 8 R3560 Paeudomonas exotoxin (.22e-0) 925 8 R3560 Paeudomonas exotoxin (.22e-0) 926 8 R3560 Paeudomonas exotoxin (.22e-0) 927 8 R3560 Paeudomonas ex	Non Dec 21 09:28:22 1998 US-08-951-733-14.zeg	### 133	Mon Dec 21 09:28:22 1998 U8-08-951-733-14.reg
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PP 11-SEP-1995. U.4.134.

PP 15-SEP-1995. U.5.013819.

PA 15-SEP-1995. U.5.013819.

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By UST/16815-498.

By UST/16815-499.

By OS-MAY-1994. 199431.

PA (ALLR) ALLERGAN 18C.

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BY HP: 98-148407/13.

BY HI: 98-148407/13.

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W08135 standard: Protein: 358 AA.
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Human cytokine response protein CR3
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RA1530 standard: Protein.

RA150 standard: Prote
RESULT 12

Wid123 standard: Procein: 398 AA.

Wid125 at an analog (irre entry)

DE Ammonifer degensia sapariste aminotransferase KC4/AA.

NA Aparists and operanderase: KC4/AA. Chiral compound.

Sammonifer degensia strain KC4.

PM 40372918-1997: 00.004.

PM 03-FMX-1996: US-546519.

PM 03-FMX-1996: US-546519.

PM 03-FMX-1996: US-546519.

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PM 03-F
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DR WFIDE: 098579

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RW-20D
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The gall gene product (P70274) is known as galactose-1-phosphate unidoltenssferase (transferase), the gall gene product (P70275) is known as unidolten diphosphatetoset 4-epimerase (ppimerase), and the galk gene product (P70275) is known as glinetase (Pimerase). And the galactokinase). The inventors claim an 1DAM molecula comprising all created of the septempres gal operon used for the expression of coreign bits in a transformed micro-oryanism.
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pp 11-NX-1395; DD0189.

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OJ-SEP-1987:
P 24-FEB-1985: US-98496.
30-FEB-1985: US-98496.
SANT ) SHJTHKLINE BERKMAN CORP.
Adams CW. Fornwald DA. Brawner ME, Schmidt FJ:
Adams CW. Fornwald DA. Contg. Streptobyces gal opp.
Prov recombinant DA. contg. Streptobyces 
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Page 32

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PF 01-JUN-1935.

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PA (CAL) | NALERE INC.

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877163 standard: Protein: 493 AA.
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PR 21.-NOV. 1991: US-99515.

PR 21.-NOV. 1992: US-995161.

PR 11.-NOV. 1992: US-99563.

PR 20 - NAY 1992: US-96629.

PA (CALJ) CACENE INC.

PA (CALJ) CACENE INC.

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R79934;
16-JMN-1996 (first entry)
Jojobs fatty-acyl-reductase: vax-synthase: jojobs: oilseed:
Patty-acyl-reductase: vax-synthase: jojobs: oilseed:
long-chain alcohol-fatty-acyl-transferase; vax ester:
transgenic plant; crop improvement: Brassica.
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R37487 atandard: Protein: 493 AA.

R47487 atandard: Cooperative and Pharmaceuticals: sperm whate.

R57487 atandard: District and Pharmaceuticals: sperm whate.

R57487 atandard: Protein: 493 AA.

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ps (CALT) - CAMENE INC.

ps (Learner MW. Met. JC. Pollard MR:

pr Psp (1958).

pr Psp (1958).

pr Psp (1958).

pr pew recombinant constructs for transforming plants of E. coli.

pr contg. nucleic acid encoding jojoba embryo long chain fatty

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411 MRPLFLE 417
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PR 17-NOV-1994 075-154792.

PR 07-DEC-1994 05-154792.

PR 07-DEC-1994 05-155310.

PR 07-DEC-1994 05-155310.

PR 11-7UN-1994 05-759310.

PR 12-7UN-1994 05-75931
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                                                                                                                                                                                                                                                                                prints one; nature to the control DNA encoding glucosyl transferase prints one; new bacterial DNA encoding glucosyl transferase from strictly rectain bighter levels of scored carbohydrates) in a form prints of the sequence special plant book in the control of the sequence represents an alpha D-glucosyltransferase from the sequence and the sequence is a surpose. A gene encoding the enzyme of the sequence of the sequence and section of sequence the control of the sequence of the sequence
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           5 B
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Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                   Query Match
Best Local Similarity 100.0%;
Matches 7; Conservative
1174 rrvgddv 1180
||||||||
164 RRVGDDV 170
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obd, from corpusbacterium glutanicum strain ooding
phesphoenolpyruvate carboxylass.
Disclosure: p. English.
ppc is important as a key entyme in the anapierotic
and increasing oxaloacetate levels, it indirectly in
levels of I-Ma.
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|621 RELSEAE 627
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Year 1812 protein
Minastch repair 1837; primer; ix
Janear; tumour; vaccine
Lachkromyces cerevisiee.
0951005-A2.
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Liphe D-glucosyltransferse: primer independent; soluble glucan;

Liphe D-glucosyltransferse: primer independent; soluble glucan;

Liphe D-glucosyltransferse: primer independent; soluble glucan;

Lucrose: transgenic plant; closing; Escherichia coli;

Mago transfer; crop improvement; blocate carbovidate; pasture;

dedsfuff; soluble glucan; blocate; Good; pharmaceutical.

Storprococcus salivarius strain ATCC 3975.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26
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6065;
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                                                                                                                                                               e 7;
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                                                                                                                                                               DB 16; Length 1577;
3.80e+01;
tches 0; Indels
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luble glucan;

Page :

151 sllrshy 157

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Mon

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SULT 32

R93469 standard: peptide: ix ....

C R93469 standard: peptide: ix ....

C R93469 standard: peptide: ix ....

T 09-MAY-1996 (first entry)

D GST-SRC protent tyrosine kinase derived peptide s3.

W ST 11gand: SHJ binding spent; bissed phage library:

W ST 11gand: SHJ binding spent; bissed phage library:

W P ST 10gand: SHJ binding spent; bissed phage library:

W P ST 10gand: SHJ binding spent; bissed phage library:

W P ST 10gand: SHJ binding spent; bissed phage library:

D 14 SEP-1995.

P 11 - MAR-1995; 003209.

P 11 - MAR-1995; 003209.

P 12 - MAR-1995; 003209.

P 13 - MAR-1995; 003209.

P 14 - MAR-1995; 003209.

P 15 - MAR-1995; 003209.

P 16 - MAR-1995; 003209.

P 17 - MAR-1995; 003209.

P 17 - MAR-1995; 003209.

P 18 - MAR-1995; 003209.

P 19 - MAR-1995; 003209.

P 19 - MAR-1995; 003209.

P 19 - MAR-1995; 003209.

P 10 - MAR-1995; 003209.

P 11 - MAR-1995; 003209.

P 12 - MAR-1995; 003209.

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P 13 - MAR-1995; 003209.

P 14 - MAR-1995; 003209.

P 15 - MAR-1995; 003209.

P 15 - MAR-1995; 003209.

P 16 - MAR-1995; 003209.

P 17 - MAR-1995; 003209.

P 18 - MAR-1995; 003209.

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P 19 - MAR-19
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ID RS
AC RS
DT 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prepared by the state of the Jak-Stat signalling pathway for indentifying inhibitors of the Jak-Stat signalling pathway for presentially useful for treating proliferative disease, esp. HTLV-1 prepared by the state of the state
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 B
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Of 24.428 1196 (first entry)

Of 24.
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Best Local Similarity 100.0%;
Matches 6; Conservative
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Best Local Similarity 100.0%;
Matches 6; Conservative
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R96119 standard; peptide: 7 AA.
R96119; R96119: R96119
18-DEC-1996 (first entry)
Reptide provides site for much sugar chain introduction olycosylation site; much sugar; N-acetyl galactosamine; therapeutic polypeptide; erythropoletin; interferon.
Synthetic.
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. No. 4.71e+02;
Hismatches 0; Indels
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. No. 4.71e+02;
Mismatches 0; Ind
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SULT 33

V41218 standard; peptide; 15 Am.

V41218 standard; peptide; 15 Am.

C v41218;

T 13-MY-1998 (first entry)

DE Tax protein fragment.

RW Tax protein fragment, HTLV-1; human T-cell leukaemia virus; hepatilis B;

RW Tax protein transcription; viral infection; genetic disorder;

RW Tax-dependent transcription; genetic disorder; genetic disorder; genetic disorder; genetic disorder; genetic disorder; genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      co high new SHI binding spents. They represent a bissed phase library control with comprises five random anno cide fanking the decapspited control was a control with the sequence of this. Which was identified as a consection sequence for the set SHI domain. These sequences were contacting the sHI domain with a mixture of the periodes under conditions contacting the SHI domain with a mixture of the periodes under conditions contacting a ligand to bind to an SHI domain to form a comprise. Any combound periodes are removed and the complexed periode ligands are discontacted from the complexes. The selected periodes are northed by contacting them with the SHI domain and then conditions or chastes the SHI domain are detected. The isolated SHI binding periodes are with the SHI domain and the conditions of chastess contacting the with the SHI domain and the conditions transitions or diseases. Once diseases include page's disease. Other conditions transition to the second state of the second state of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF 01-NOV-1995, JP-22318.

PR 01-NOV-1994, JP-225111.

PR 01-NOV-1994, JR-22511.

PR 12-1994, JR-22511.

PR PPPLIS-1994, JR-22511.

PR PPLIS-1994, JR-22511.

PR PPLIS-1994, JR-22511.

PR PPLIS-2994, JR-22511.

PR PPLIS-2994.

PR PPLIS
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Matches 6: Conservative
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Dest Local Similarity 100.0%;
Matches 6; Conservative
W09703358-A1.
30-JAN-1997.
02-JUL-1996; (
07-JUL-1995; (
(USSH ) US DEI
Leonard WJ;
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R71V: transactivating protein. Tax, peptide fragment #36.

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R71V: transactivating protein. Tax; regulator: host

R71V: transactivating protein.

R71V: transactivating protein.

R71 binding site: target molecule.

R81 binding site: target molecule.

R81 binding site: Location/Qualifiers

R81 binding site: 10

R81 binding site:
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A W1230. Standard: Peptide: 15 AA.

W1230. PS Not High (first entry)

DE SOCIETY (First
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They provide a poverful se
of ligands with the same of
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The inhibitors can be used to inhibit transcription of DNA, that codes for proteins that can be harmful to mammals, especially humans, e.g. to treat viral indections (e.g. https://doi.org/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.j.com/10.1001/j.com/10.1001/j.com/10.1001/j.com/10.1001/j.com/10.1001/j.com/10.1001/j.com
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67 AAFRAL 72
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R74374 standard: peptide: 4...

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OF HTU-NN-1996 (first entry)

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OF HTU-NN-1996 (first entry)

KW HTU-1 associated myslopath;

KW HTU-1 associated myslopath;

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PD 10-KNY-1995.

DP 06-KNC-1993: 103742.

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PHOREM 1997A.

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B. Geterrhalis CD epicope containing oligopeptide.

B. Geterrhalis CD epicope containing oligopeptide.

B. Conterrhalis Enchancella catarrhalis: vaccine: epicope: otitis media.

RW CD protein Enchancella catarrhalis:

RW CD protein Enchancella catarrhalis.

RW CD protein Seriabasis.

PR 20-SEP-1994: U19932:

PR 20-SEP-1994: U1994: U1994
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Tax protein fragment, HTLV-1, human T-cell leukamia vitus; hepatitis B;
Tax protein fragment, HTLV-1, human T-cell leukamia vitus; hepatitis B;
human lymphotropic vitus; tenna-activating factor inhibitor; therapy;
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Humanypous failial hypercholasterolaemii; cancer.
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1929 standard: Protein: 21
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pp 10-FB-199408.

pp 10-F Query Match 0.6%; Best Local Similarity 100.0%; Matches 6; Conservative Query Match 0.6%; Best Local Similarity 100.0%; Matches 6; Conservative New MTLV-I antigenic peptide(s): - used for disgnosing MTLV-I intertion(s) pattic. MTLV-I associated myelopsthy and adult T-cel lenkenis.

Example 1: Columns 11-12: 21pp; English

Example 1: Columns 11-12: 11pp; English

PR(1856-PR375 are human T-cell lymphotropic virus type I (HTLV-I)

PR(1856-PR375 are human T-cell lymphotropic virus type I (HTLV-I)

PR(1856-PR375 are human T-cell lenkaemia, and HTLV-I, e.g. adult T-cell lenkaemia, and HTLV-I, sequence 20 AA) 3 psflls 8 ||||||| | 365 psfLLs 370 12 pails 17 |||||| | 365 PSFLLS 370 09:28:22 Score 6: DB 14: Length Pred. No. 4.71s+02; O; Mismatches 0: Ind Score 6; DB 28; Length Pred, No. 4.71e+02; O; Mismatches O; Ind 20: 0 0

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Score 5: DB 27: Pred. No. 4.71e+02 0: Mismatches

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Synthetic property.

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ul987s standard: peptide: ...
ul987s; sequence for use in Tlymphocyte veto molecule.
Ladder sequence for use in Tlymphocyte veto molecule: ladder seq
Tlymphocyte veto molecule: chineric molecule: ladder seq
Tlymphocyte veto molecule: ophineric molecule: ladder seq
targetting polypeptide: suppression: immune response: transplant rejection.
transplant rejection.
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12 : WAY 1998 (first entry)

12 : WAY 1998 (first entry)

13 : WAY 1998 (first entry)

14 : WAY 1998 (first entry)

15 : Al dopamine receptor antagonist.

16 : WAY 1998 (first entry)

17 : WAY 1998 (first entry)

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DI 17-DEC 1996 (first entry)

Received the coupled codezant receptor 17 N-terminal sequence.

RW echicophrenia department cAMP adenosite; thrombin; address; copsin;

RW addrant; cytomegalovinus; errotometylc.

RW docant; cytomegalovinus; servicentylc.

RW docant; cytomegalovinus; servicentylc.

RW docant; cytomegalovinus; servicentylc.

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//note *optionally in D form or absent,
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either terminal hydrogen can be
independently abbettured with 1-12c alkyl,
1-20c phenylakkyl, 11-30c naphthylalkyl,
1-10c hydroxynaphthylalkyl or 500H
1-10c hydroxynaphthylalkyl or 500H
X= 1-12c alkyl, 7-20c phenylalkyl, 11-20c
naphthylalkyl, 1-12c hydroxynaphthylalkyl, 7-20c
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/label Ala, Aib, e 21
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The Wossiles, M.

PR 11-027-1965; UO4582.

PR 14-NP-1995; UO4582.

PR 14-NP-1995; UO4582.

PR 16-SEP-1995; UO4582.

PR 16-SEP-1995; UO4582.

PR 16-SEP-1995; US-22337.

PA (TULA) TILLNEE EUGLATIONAL FUND.

PA (TULA) 
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treatment of Ho
the DNAs can be
mammal against
Sequence 32;
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f HCV infection. The peptide
n be used in the preparation onst HCV infection.

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Abu Abu, bla, His OTEER
Anotes "OTEER" 5-mainopentanoic acid,
optionally absent:

7 Abel Aib, Ala. 4Abu, His
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optionally absent;
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terminal calboxyl or NWT-T-CET Z:
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8 alfavl 13
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                                                                                                                                          acid sequences predicted from various OFF were analysed for significant homology to other known or exported membrane protesins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production. e.g. in E. coli hosts.
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SUNGMARY \$87-1291 64,150,161,207,211, 218,251,256,290, 311,322,347,416, 427,457,489,520, \$56 846 840

*binding_site carbohydrate (Asn) (covalent) *status predicted\
*active_site Cys (phosphocysteine intermediate) *status predicted\
*binding_site substrate phosphate (Arg) *status predicted
*length 1291 *molecular-veight 144601 *checkaum 8574

Oesy Match 0.9%; Score 9; DB 2; Length 1291; Best Local Similarity 100.0%; Pred. No. 974e-04; Matches 9; Conservative 0; Nismatches 0; Indels 0; Caps

Db 8 LAFGFALLD 16 ||||||||| Oy 119 LAFGFALLD 127

ACCESSIONS REFERENCE eauthors ejournal etitle ORGANISM DATE RESULT ENTRY TITLE Remmings, B.A.: Schwart, K.: Adavani, S.R.: Jans, D.A. (FEBS Lett. (1986) 203:119-212
Expression cloning of a cloth encoding the type II regulatory aubunit of the cAMP-dependent protein kinase. Loca MUD:87080763 A28652 etype fragments
protein kinase (EC 27.1.37), cAMP-dependent, type II-alpha
regulatory chain - pig (fragments)
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10.4mr.1988 (sequence_revision O5-Mar-1993 *text_change
26.7mr.1986 (sequence_revision O5-Mar-1993 *text_change
26.7mr.1986 (1477); A15740

Potter, R.L.: Taylor, S.S.
J. Biol. Chem. (1979) 234.9000-9005
Correlation of the Akb binding domain with a site of autophosphorylation on the regulatory subunit of

Mon Dec 21 09:28:23 1998

ENTRY
TITLE
ORGANISH
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#gene 59
CLASSIFICATION #superfamily uracil-DNA glycosylase
KETMORDS 91/cosidase: hydrolase
SUMMARY #length 105 #mplecular-veight 34376 #checksum

Caps

Osty Match Osmilarity 100 0%; Score 8: DB 1: Length 305; Best Local Similarity 100 0%; Pred. No. 1 39e-01; Matches 8; Conservative 0: Hismatches 0; Indels 0;

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ACCESSIONS REFERENCE Sauthors Sjournal Ftitle ecross-references MUID:87113002
eaccession A26592
esmolecule_type DNA
esresidues 1-342 eslahal Tiel. J.: Stocking. C.: Stacey, A.: Ostertag, W.

- Viril. (1987) 51:889-87

- Cemperature-sensitive mutant of the mysloproliferative
sacrosa virus, altered by a point mutation in the mos
sacrosa virus, been modified as a selectable retroviral DNA 1-342 selabel FRI

US-08-951-733-14.rpz

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Page 27

FEATURE 61-341 69-77 90 SUMMARY

Db 291 LRPSLTGA 298 |||||||| Cy 372 LRPSLTGA 379

kio, K.: Smith, S.B.: Krebs, E.G.: Walsh, K.A.: Titani, K. cochemistry (1984) 33:4200-4205 to the content of bovine type in acid sequence of the regulatory subunit of bovine type II adenosine cyclic 3',5'-phosphate dependent protein

enccession A0 MUID: 85023306

ecross-references MDID:91378531
saccession 617059
serolducale_type protein
seresiduce 1155-166 setabel 88A
serolduce 1155-166 setabel 88A

Page 25

Page 26

CAMP-dependent protein kinase II from porcine skeletal ecross-reference muclei ecross-reference muclei ecross-reference muclei ecross-reference muclei ecrossia (n. 1970) ecrossia ecrosia (n. 1970) ecrossia ecrosia experiore ecrossia (n. 1974) estabel por experiore ecrossia ecrossi

CLASSIFICATION KEYWORDS cAMP binding: duplication: heterotetramer: homodimer: phosphoprotein; phosphotransferase superfamily cAMP-dependent protein kinase regulatory chain: cAMP receptor protein cyclic nucleotide-binding domain

FEATURE 81-155 #domain cAMP receptor protein cyclic nucleotide-binding domain homology (fregment) #label CAP #length 169 #check&um 765

SUMMARY Osery Match
Oss; Score 8: DB 2: Length 169:
Best Local Similarity 100 0%; Pred, No. 128-01;
Matches 8: Conservative 0: Mismatches 0: Indels 0 Caps

RESULT 5

US-08-951-733-14.

GENETICS RECEDENCES GB:M15424: NID:g332210; PID:g332211
GENETICS
Sene mos
cLASSIFICATION superfamily kinase-related transforming pro KEYWORDS mos
superiamily kinase-related transforming protein; protein
kinase homology
ATT; oncogene: phosphotransferase; serine/threonine-specific
protein kinase; transforming protein

#domain protein kinase homology #label KIN\
#region protein kinase ATP-binding motif\
#active_site Lys #sectus predicted
#length 342 #molecular-weight 37970 #checksum 8888

opery Mach Similarity 100.0%; Score 8; DB 1; Length 342; Best Local Similarity 100.0%; Pred No. 129-01; Maches 6; Conservative 0; Mismatches 0; Indels 0; Gaps

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ACCESSIONS REFERENCE sauthors sjournal stitle ORGANISM DATE RESULT ENTRY TITLE OKBOAR **type complete
protein kinase (EC 2.7.1.17), cAMP-dependent, type II-alpha
regulatory chain bowine
*formal_name dos prinigeniue kaurus *common_name cattle
formal_name dos prinigeniue kaurus *common_name cattle
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tip-drt.1982 *sequence_revision 15-Oct-1982 *text_change
19-may-1992.

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COMMENT

COMMENT chains and two catalytic chains. Activation by other produces we active catalytic monomers and a repulatory differ that blads four cathy molecules.

Four types of regulatory chains are found: I alpha. I beta, II beta, II beta, II beta, II beta, II beta, II cathy and III beta. That are the pression varies among tissues and II alpha, and III beta. That are phosphorylated by the activated of the production of the activated phosphorylated by the activated phosphorylated by the activated phosphorylations by that thighcal significance of phosphorylations by the thigh cathers association by binding to amboring proceins, including the MAP Athras. The ambion process in including the MAP Athras. The

Keywords perfamily cAMP-dependent protein kinase regulatory chain: ted amino end; cAMP binding; duplication; ptetramer; homodimer; phosphoprotein;

*domain protein interaction alabel DIPA

*domain AMP receptor protein cyclic nucleotide-binding

*domain Ampology #label CAIA

*domain Ampology #label CAIA

*domain Ampology #label CAIA

*modified_afte activated anno end (Ser) *status

*experimentalA

*proline-directed kinase) *status predicted

*binding_afte phosphate (Thr) (covalent) (by

proline-directed kinase) *status predicted

*binding_afte camp (colu, any) *status predicted

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Score 8; DB 1; Length 400; Pred. No. 1.29e-01; 0; Mismatches 0; Indels 0; Gaps 0

OKHUJR Ptype complete protein kinase (CC 27.1.17), cAMP-dependent, type II-alpha regulatory chain - human eformal_name man spicins ecommon_name man eformal_name man second spicins ecommon_name man that change 07-Ker-1993 secquence_revision 31-Ker-1993 stext_change 07-Ker-1993 secquence_revision 31-Ker-1993 stext_change

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Egene
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452 poscol
superfamily cytochrome P450
heme: steroid binding

SUMMARY

Db 128 PYGVLLKT 135 |||||||| Qy 426 PYGVLLKT 433 0;

US-08-951-733-14. IPI

O.8%; Score 8; DB 1; Length 404; Best Local Similarity 100.0%; Pred. No. 1.29-01; Indels 0; Gaps Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps ္ပ

sbinding_site heme iron (Cys) (axial ligand) estatus predicted elength 508 emolecular-weight 58195 echecksum 7347

Ouery Match 0.8%; Score 8: DB 2: Length 508; Best Local Similarity 100 0%; Pred. No. 1280-01; Padels 0; Manatches 0: Indels 0;

10 HRBYSI etype complete
dnaK-type molecular chapetone SSCl precursor, mitochondrial
yeast (Saccharemyces cetevisiae)
endonuclease Scel 75K chain: endonuclease Scel large chain:

ALTERNATE_NAMES

ACCESSIONS
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sauthors
sjournal
title ORGANISM DATE 05 110 EEEDTOPR 117 [[1]||||| Qy 461 EEEDTOPR 468 FEATURE 1-134 135-256 CLASSIFICATION Dec 21 09:28:23 1998 Query Match 0.8%; Best Local Similarity 100.0%; Matches 8: Conservative 48,211 95 257-389 empalecule type mRM. **reakdusa 1-508 s1abel NOK **reakdusa 1-508 s1abel NOK Nomura, O.: Nakabayashi, O.: Nishimori, K.: Misuno, S. Gene (197) 185:117-222
The cDNA cloning and transient expression of a chicken gene encoding cytochrome P-450sec.
Addensi gland
J6200 slength 404 smolecular-weight 45518 schecksum 9820

> Mon Dec 21 09:28:23 1998 US-06-951-733-14.zpr

Page 31

Craig, B.A.: Kramer, J.: Shilling, J.: Werner-Washburne, M.: Slower, S.: Roselcoshing, J.: Werner-Washburne, M.: Slower, S.: Roselcoshing, J.: Werner-Washburne, M.: Scotland, Roselcoshing, Roselcosh heat shock protein 70-related protein SSC1; protein GTF654; protein J1639; protein TJR045c formal_name Saccharomyee ectevisioe 0-Uni-1992 secquence_revision 30-Uni-1992 stext_change 10-Jnn-1988

ACCESSIONS REFERENCE Sauthors ORGANISM DATE

authors Hilliam, N.; Nakagaw, K.; Yamamoto, C.; Shibata, T.
ejournal J. Biol. Chem. (1990) 265;1519-15197

Fittle A subunit of yeast site-specific endonuclease Seel is a
miconhomital version of the 70-NDA heat shock protein.

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#molecula_type protein
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#Authors Scheer, P.E. Krieg, U.C.: Hwang, S.T.: Vestweber, D.:
#Authors Scheer, P.E. Krieg, U.C.: Hwang, S.T.: Vestweber, D.:
#FOURNAL ECONOMIC AND PROTEIN PARTLY translocated into yeast
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#Itle A protein PROPERING TO A 70 Kd mitochondrial stress
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September

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Mon Dec 21 09:28:23 1998

Page 29

US-08-951-733-14. rpr

Page 30

SO3885 SO3885 Oryen, O.; MyXlebust, F.; Scott, J.D.; Hansson, V.; Jahnsen,

ACCESSIONS REFERENCE Pauthors

TISS Lett. (1989) 246:57-64
Ruman reagia oDNA for the regulatory subunit RIT-alpha of cNP-dependent protein kinase encodes an alternate anino-terminal region.

none MyD:8931141)

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expeditions 1.404 without and a regulatory diagraph of the entyme is composed of two regulatory of the entyme is composed of two regulatory that inactive form of the entyme is composed of two regulatory two continuous two structures and a regulatory diagraph bands four extensions of the continuous active catalytic monopers and a regulatory diagraph bands four extensions of the continuous conti

Couly molecular control of the state of the policy process of regulatory chains are found: I alpha, I beta, four types of regulatory chains are found: I alpha, I beta, and II beta. Their expression waries among tissues and II alpha the state of the sta

*gene GDB:PRANARA

**Cross-references GDB:120314; ONIM:176910

*map_position 'pter'/p22

CLASSIFICATION **superfamily cAMP-dependent processing the process of the process *superfamily cAMP-dependent protein kinase regulatory chain: cAMP receptor protein cyclic nucleotide-binding domain

KEYWORDS omology tyjated amino end; cAMP binding; duplication; heterotetramer; homodiner; phosphoprotein; phosphotransferase

FEATURE 2-404 261-393 2-138 139-260

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Analysis of a 43.5 kb DNA sequence of chromosome X reveals three CRNA genes and 14 new open reading frames including a gene most probably belonging to the family of ubiquitin protein ligages.

Page 33

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eaccession 529069
estatus preliminary
esmolecule_type_mRRA
esresidues 1-970 sslabe
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highly homologous to inositol polyphosphata-5-phosphatase.

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escross references EMBL:X79743
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thors Voss, R.; Tamames, J.;
                                                                                                                                  Voss, H.; Tamames, J.; Teodoru, C.; Valencia, A.; Sensen, C.; Wiemann, S.; Schwager, C.; Elmermann, J.; Sander, C.; Ansorge, W. Sensen, S.; Schwager, C.; Elmermann, J.; Sander, C.; Ansorge, W. Sensen, S.; Sander, C.; Ansorge, W. Sensen, S.; Sander, C.; Sander, C.; Sander, C.; Sander, C.; Vasar Chromosome IX.
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Shimasaki, S.; Gao, L.; Shimonaka, M.; Ling, N. Nol. Endocrinol. (1991) 5:938-948
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Blochem. Blophys. Res. Commun. (1991) 181:1131-1136
Honthication and NH2-terminal anno acid sequence of three
Insulin-like growth factor-binding proteins in porcine
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ALTERNATE_NAMES protein TiBGC: protei
                                        RESULT 15
ENTRY
TITLE
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No. 1.29e-01; Tindels 0; Gaps Matches 0; Conservative 0; Missatches 0; Indels 0; Gaps
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Matches 7; Conservative 0; Mismatches 0; Indels
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*cross-references MUID-93049376
*accession D20734*
**section D2074*
**section D2
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submitted to the EMBL Data Library, August 1994
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slength 39 *molecular-veight 4313 *checksum 1192
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hypothetical J.18 protein (trnR-rps15 intergenic region)
rice chloroplast
formal_name chloroplast Oryza sativa ecommon_name rice
11-Mar-1990 sequence_revision 11-Mar-1990 etext_change
n11-Mar-1990.
          901945 etype fragment myosin catalytic light chain, ventricular and slow striated
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40; $30889; $58706; $50795; $27443
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**Cross-references MUID:86043655 **Accession A33129 **Accession A33129 **Constitution A33129 **Classification A33129 **Classif	ALTERNATE_NAMES systematic mouse (fragment) OCGANISM OCCANISM O	Non Dec 21 09:28:23 1998 US-08-951-733-14.pp
	Page 39	Page 37
Past Local Similarity 100.0%; Pred. No. 1.04e+01; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Db 46 AVVIEOS 52 Oy 811 AVVIEOS 817 RESULT 20 REWITA stype complete Tifle T-cell receptor Alpha Chain precursor V region (CTL-LLT) . ORCANISM stormal_name Homo aspins Scommon_name man DATE 17-Mar-1987 sequence_revision 17-Mar-1987 stext_change O2-Sep-1997 ACCESSIONS A22016	Chery Match silenitry 100.7% Score 7, DB 2, Length 52; Bast Local Scalarity 100.0% Prod Mo 1 (04+************************************	Mon Dec 21 09:28:23 1998 US-08-951-733-14.rpr

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RESULT 21 ENTRY TITLE ORGANISM DATE *Accession 530280

**real-dues 1-148 **Albel ROP 239854; PID:9298655

**Created Feterence 681-556552; NID:9298654; PID:9298655

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Gen Genet (1991) 2017-2012-20
Eacherichia coli C homoprotocatechwate degradative
peron: hpc gene order, direction of transcription and
on crol of expression.

O.7%; Score 7; DB 2; Length 148; Best Local Similarity 100.0%; Pred. No. 1.04e-01; Indels 0; Gaps Matches 7; Conservative 0; Mismarches 0; Indels 0; Gaps hpcR DNA binding: transcription regulation elength 148 #molecular-weight 17255 #checksum 5904 9

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ITTLE hypothetical protein FLL042c - yeart (Saccharomyces tritte)

ORGANIZE hypothetical protein L0737

ORGANISH OLANG-1986 Saccharomyces cerevisiae

OLANG-1987 SACCHAROM-1987 Salonile Type DNA Teafous Type DNA Cross-Teferences DOB::773147; NID:91160215; PID:e245470; PID:91160217; Wedler, H.; Wedler, E.; Scharfe, M.; Wambutt, R. submitted to the Protein Sequence Database, May 1996 864794

Mon Dec 21 09:28:23 1998

US-08-951-733-14.rpr

RESULT 24 ENTRY TITLE ORGANISM DATE

ACCESSIONS REFERENCE *Authors *journal *title

GENETICS sgene FEATURE 2-174 SUMMARY

Length 174;

RESULT 25 ENTRY TITLE ORGANISM DATE ACCESSIONS REFERENCE Fauthors

697 LLGASVL 703 Hishids, T., Iwasaki, H.; Ishioka, K.; Shinagawa, H. Gone (1995) 182-03-70
Nolecular analysis of the Pseudomonas arruginosa genes, ruwa, ruwa and ruwc. Involved in processing of homologous recombination intermediates. CS478 type complete - Pacudomonas aeruginosa ndodeoxyribonuclease rucc - Pacudomonas aeruginosa formal_name Pacudomonas aeruginosa eruginosa - 7.011:1997 sequence_revision_39-Aug-1997 stext_change - 7.91:1997-1997 sequence_revision_39-Aug-1997 stext_change - 7.91:1997-1997 sequence_revision_39-Aug-1997 stext_change

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**Insolectic_type DNA

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**Cress-references DDB::D83180: NID:g1183837; PID:d1012484; PID:g1183840

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product endodeoxyribonuclease ruvC estatus predicted elabel MAT estatus predicted elength 174 emblecular-veight 19556 echecksum 8754

Db 164 GARRRGG 170 1111111 Qy 242 GARRRGG 248 Ouery Match 0 7%; Score 7; DB 2; Length 174; Best Local Similarity 100.0%; Pred. No. 1 (04+0); Matches 7; Conservative 0; Himatches 0; Indels 0; Gaps

\$1,240 "type complete
yop20 protein 'Terainia enterocolitica
formal_namo 'Terainia enterocolitica
cormal_namo 'Terainia enterocolitica
protein 1944 esequence_revision 10-Nov-1995 ftext_change
09-Sep-1997 ichhels, T.; Mattiau, P.; Brasseur, R.; Ruysschaert, J.M.; Cornelia, G. Theet Immun, (1990) 58:2840-2849 eecretion of Yop proteins by Yersiniae. me MOID:9034644

Mon Dec 21 09:28:23 1998

US-08-951-733-14.xpz

Page 43

#accession 51420 #accession preliminary #molecule_type DNA #residues 1-102 ##label NIC:948602; PID:948604 ##CTOSS-references EMBL:X52733; NID:948602; PID:948604 \$14240

yop20 elength 182 #molecular-veight 20828 #checksum 1492

GENETICS

O.7%; Scote 7; DB 2; Langth 182; Best Lowards Smilarity 100 0%; Pred No. 104e+01; Matches 7; Conservative 0; Hismatches 0; Indels 0; Gaps

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62 GSILSTL 68 . |||||||| 856 GSILSTL 862

ENTRY HORTLY stype complete
TITLE myosin siteati light chain 3, ventricular and slow skeletal
muscle : ret
mu RESULT 26 ENTRY TITLE ; \$15759; \$06169

ACCESSIONS REFERENCE *authors *journal *citle KcHally, E.M.: Buttriek, P.M., Leiswand, J.A.
Nucleic Acids Res. (1989) 1872753 278678
Ventricular myosin light chain 1 is developmentally regulated
and does not change in hypertension.
rgs. NutD-89340011

*accession \$15759

*accession \$15759

*residues 1-200 *slabel PE2

*accession BDU::N18315; NID:956671: PID:9763179

*accession BDU::N18315; NID:956671: PID:9763179

*antrons 40/1: 50/1: 100/1: 166/1: 192/1 *cross-reference MUID:89240031
*moclecule_type mRNA
*moclecule_type mRNA
*residues 1-200 *slabel MCN
*residues 1-2 etitle Perissany, M.; Wadgaonkar, R.; Kumar, C.; Martin, B.J.; Siddkyli, M.A.Q. Nucleic Acids Res. (1989) 17:7733-7734 Characterisation of a rat myosin alkali light chain gene expressed in ventricular and slow twitch akeletal muscles. 515759

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Page 42

Mon Dec 21 09:28:23 1998

Page 41

stexperimental_source strain S288C GENETICS *map_position 12L SUMMARY slength 167 *molecular-veight 19759 *checksum 3500

O.7%; Score 7; DB 2: Length 167;
Best Local Similarity 100.0%; Pred. No. 1.04e+01;
Matches 7; Conservative 0; Minmatches 0; Indels 0; Gaps 9

ORGANISM DATE RESULT 23 ENTRY TITLE Sod916 *type fragment
T-ceil receptor delta chain precursor V-D-J region (clone RT08), - human (fragment) ecomon_name man formal_name incomon_name man 10-Sep-1991 *sequence_revision 30-Sep-1991 *text_change 08-Sep-1997
08-5p-1997

ACCESSIONS REFERENCE Sauthors stitle Takihara, Y.; Reimann, J.; Hichalopoulos, E.; Ciccone, E.; J. Exp. Ned. (1989) 165:393-405 Diversity and structure of human T cell receptor delta chain genes in peripheral blood gamma/delta-bearing T lymphocytes

*cross-references MID-8004339
*accession 504316

edomain signal sequence status predicted slabel SIC\
sproduct reall receptor delta chain (fragment) status
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Score 7: DB 2: Length 168; Pred. No. 1.04e+01; 0; Mismatches 0: Indels Caps

Query Match 0.7%; Best Local Similarity 100.0%; Matches 7; Conservative

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4 LLGASVL 10

Mon Dec 21 09:28:23 1998	1998	US-08-951-733-14.rpr
CLASSIFICATION	*superfamily calmodulin; co	almodulin repeat homology
REYWORDS FEATURE	blocked amino end; calcium binding; cardiac muscle; duplication: EF hand: muscle contraction; skeleta.	ocked amino end; calcium binding; cardiac muscle; duplication; EF hand: muscle contraction; skelotal

SUMMARY Db 30 AAPEPER 36 ||||||| Qy 264 AAPEPER 270 O-TY, Score 7; DB 1; Length 200; Best Local Similarity 100.0%; Pred. No. 1.06+01; Indele 0; Gaps Maches 7; Conservative 0; Milmatches 0; Indele 0; Gaps 54-88 133-165 168-200 sdomain calmodulin repeat homology slabel EPN adomain calmodulin repeat homology slabel EPN adomain calmodulin repeat homology slabel EPN adomain calmodulin repeat homology slabel EPA adomain calmodulin repeat not compared the blocked amino end (Pro) (in mature form) seaters predicted states predicted states and seaters predicted states and seaters are seaters. muscle

RESULT 27
ENTRY
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ni, G.; Azevedo, V.; Bertero, M. Hellado, R.P.; Misuno d.; Moone, D.; O'Reilly B.; Park, S.H.; Parro, ster, L. Brans
unilet, S.
uniter, N. J.
Cummings, N. J.
Exrigon, J.
C.: Fulta,
C.: Fulta,
J. Grandt,
J. Grandt,
J. Harvood
Hosono, S.
Rosono, N.
Karanta, D.
Karanta, D.
Kamano, M.

SUMMARY FEATURE 1-163, 195-261 **ccession A03926

**spolecul_type DNA

**residues 1-251 **slabel DIJ early ElA protein
CLASSTFICATION **superfamily adenovirus early ElA protein
Extraority splicing: DNA binding: early protein;
CLASSTPICATION **creative splicing: DNA binding: early
creative splicing: early early
classification of the creative splicing: early
creative splicing: early early
creative splicing: early early
creative splicing: early
cre eproduct early E1A 24K protein setatus predicted slabel E4K 8 molecular-weight 28185 schecksum 884

ACCESSIONS REFERENCE Fauthors pr-1997 #sequence_revision 25-Apr-1997 #text_change , T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamitu, E.; mura, Y.; Hiyalima, N.; Hiktosawa, M.; Sugiara, M.; muto, S.; Kimura, T.; Hesouchi, T.; Matuno, A.; muto, S.; Nakasaki, N.; Maruo, K.; Okumura, S.; Okimpo, Takuchi, C.; Mada, T.; Watanabe, A.; Tamada, M.;

CLASSIFICATION KEYWORDS FEATURE

US-08-951-733-14. rps

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overy Match 0.7%; Score 7; D8 1; Length 261; Best Local Similarity 100.0%; Pred No. 104e+01; Best Local Similarity 100.0%; Pred No. 104e+01; Andrew 0; Gaps

RESULT 29 ENTRY TITLE ORGANISH OVARIETY DATE

Page 47

Mon Dec 21 09:28:23 1998

SUMMARY 33-149 88

#domain response regulator homology #label RRHN binding_site phosphate (Asp) (covalent) #status predicted #domain=response #d

ouery Match 0.7%; Score 7; DB 2; Length 262; Best Local Similarity 100.0%; Pred. No. 1.04e+01; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 142 LEELVAR 148

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Gy 99 LKELVAR 105

ORGANISM DATE REFERENCE 00/17/ etype complete
alpha-tocophetel transfer protein - human
eformal_name Namo sepiens ecompon_name man
21-bec-1990 sequence_revision 06-Jun-1997 etext_change
10-0ct-1997
c0.1727: 52146

submitted to the EMBL Data Library, February 1995 G01727

tus preliminary: translated from GB/EMBL/DDBJ Geula_type mRNA idues 1-728 selabel DEN se-references EMBL:U21938; NID:g726181; PID:g726182 Ouahori, K.: Arita, H.; Rayden, H.; Hentati, F.; Hamida, H.B.; Sokol, R.; Arai, H.; Inoue, K.; Handel, J.L.; Koenig, H.

opurnal Nature Genet. (1995) 9:141-145
etitle Asaxia with isolated vitamin E deficiency is caused by mutations in the alpha-tocopherol transfer protein.
essentus \$23466
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O.7%: Score 7; DB 2; Length 278; Seet Local Similarity 100.0%; Pred. No. 1.04e+Ol; Maches 7; Conservative 0; Mismacches 0; Indels 0; Gaps

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Page 45

Mon Dec 21 09:28:23 1998

e, Y.; Sato, T.; Scanlon, E.;
A.; Scoffone, F.; Sakiguchi, J.;
Serror, P.; Sakiguchi, J.;
E.; Takagi, T.; Takahashi, H.;
H.; Tanakoshi, A.; Tanako, T.;
H.; Tanakoshi, A.; Tanako, T.;
Tro, V.; Ochiyana, S.;
Trot, V.; Ochiyana, S.;

patte, P.; Toy...er,
patte, P.; Yannier,
ndenbol, M.; Yannier,
sabutt, R.; Pedier, E.; Wedle.,
sabutt, R.; Pedier, E.; Wedle.,
kitters, P.; Yannier,
K.; Yes, K.; Yoshida, K.; Yoshikava, H.F.; ...
Yoshikava, H.; Danchin, A.
Yoshikava, H.; Danchin, A.
"A gequence of the Gram-positive bacterium
"ota gequence of the Gram-positive bacterium
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Nature (1997) 390:24 The complete genome Bacillus subtilis.

otery Match 0.7%; Score 7; DB 2; Length 205; Best Local Similarity 100.0%; Pred No. 1.04e-0; Gaps Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps ydhK elength 205 *molecular-weight 22536 *checksum 3012

Db 105 VTGAYDT 111
0y 735 VTGAYDT 741

RESULT 28
ENTRY
TITLE
CONTAINS
ORGANISM WAAD87 stype complete
early ELA 28K protein - human adenovirus 7
early ELA 24K protein
stormal_name Mastadenovirus h7 scommon_name human adenovirus

9note 18-Dec-1981 *sequence_revision 18-Dec-1981 *text_change 16-Feb-1997

ACCESSIONS REFERENCE Sauthors eauthors Dilkema, R.; Dekker, B.M.M.; van Ormondt, H.; de Waard, A.; Boyer, B. H.W.; sournal Gene (1980) 12:207-29; etitle Gene organisation of the transforming region of weakly scross-references MUID:81237793

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1998

RESULT ENTRY TITLE ORGANISM DATE

ACCESSIONS REFERENCE Fauthors

smap_position CLASSIFICATION FEATURE 53-247

SUMMARY

U8-08-951-733-14. rpr

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Authors Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamitu, E.;

***Rammora, Y.; Hiyajiam, N.; Hitosava, M.; Sugiura, N.;

***Saamoto, S.; Kimura, T.; Hosouchi, T.; Natano, A.;

***Muraki, A.; Natasaki, N.; Naruo, K.; Okumura, S.; Shipo,

5; Takeuchi, C.; Wada, T.; Watanaba, A.; Tanada, K.;

**Journal DNA Res. (1996) 3:109-13 erome of the uncellular

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secross-references GDB:51354; OMTH:600415

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**cross-references GB:D49488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arita, M.; Sato, Y.; Miyata, A.; Tanabe, T.; Takahashi, Kayden, M.(1) Arit. M.; Inous, K.
Blochem, M. (1995) 306:437-44,
Haman alpha-toopperbt transfer protein: cDNA cloning, sefficient and chromosomal localization.
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in . Synechocystis sp. (PCC 6803)
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*journal Nuclectice Ress. (1991) 19:3742

*title Nuclectice sequence of a novel diverged human homeobox gene

*cross-references MUD:91305125

*accession $15651 | 19:3742

*accession prelimin-----
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Fraser, C.M.: Sadov, P. S. Mason, T.M.: Oleen, G.J.: Fraser, C.M.: Santth, M.O.: sjournal Nature (1997) 390; 364-370

**Sitle The complete genome asquence of the hyperthermophilic, recession sulfater-reducing archaeon Archaeoglobus fulgidus.

**Gross-references MyID:98049343

**Accession 895337

**Situation of the hyperthermophilic, P. S. Marcellin, MyID:98049343

**Accession 895337

**Situation of the hyperthermophilic, P. S. Marcellin, MyID:98049343

**Accession 895337

**Situation of the hyperthermophilic, P. S. M.: Sadov, P. S. M.:
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submitted to the EMBL Data Library, September 1990
DNA sequence analysis of the replication region of the
Pseudomonas acruginosa plasmid 891-5.
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Rétch, C.T.; McKell, L. K.; Badger, J.H.; Glodek, A.; Abou, L.; Overbeek, R.; Goosyne, J.D.; Mcidan, V. Hoonald, L.; Utterback, T.; Cotton, M.D.; Spriggs, J.F.; McCoonald, L.; Utterback, T.; Sykes, S.H.; Sadov, P.H.; P.; Attioch, P.; Maine, B.P.; Sykes, S.H.; Sadov, P.H.; D'Andres, R.P.; Bowmann, C.; Fylif, C.; Garland, S.A.; Mason, T.K.; Olsen, G.J.; Fraser, C.N.; Smith, N.O.; Woese, M.S.; C.; Garland, S.A.;
                                                                                         attner, F.R.; Pluntett III, G.; Bloch, C.A.; Perna, H.T.;
Burland, V.; Rilay, M.; Collado-Vides, J.; Glasner, J.D.;
Rode, C.R.; Myhav, G.F.; Gregor, J.; Davis, N.W.;
Rode, C.R.; Myhav, G. Goeden, H.A.; Rose, D.J.; Nau, B.; Sha
Kirkpatrick, H.A.; Goeden, H.A.; Rose, D.J.; Nau, B.; Sha
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J.: Rerv. J. N. 197, 135-7125

**Litle Complete genome sequence of Methanobacterium comparative genomics.

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Dubois, J.; Aldredge, T.; Bashiradch, R.; Blakely, D.;

COO., R.; Gilbert, R.; Harrison, B.; Heany, L.; Keegle, P.;

COO., R.; Gilbert, G.; Charrison, B.; Januari, R.;

Loo., R.; Gilbert, G.; Charrison, B.; Januari, H.;

Laman, Y.; Mirrison, G.; Goyal, A.; Pietrokovski, S.;

Kodougali, S.; Shimer, G.; Goyal, A.; Pietrokovski, S.;

Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling,
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conserved hypothetical protein MTH894 - Methanobacterium
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Mol. Pharmacol. (1994) 46:211-220
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                                                                                                                                                           Adams, C.M.; Fornvald, J.A.; Schmidt, F.J.; Rosenberg, M.;
Brawner, M.E.
J. Bacteriol. (1988) 170:203-212
Gene organisation and structure of the Streptomyces lividan
94.0 person.
coes MUID:89086869
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KEYMORDS ATP; galactose metabolism: phosphotransferase
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ubiquinol-cytochromec reductase (EC 1.10.2.2) cytochrome b
- jelly fungus (Trimorphomyces papilionaccuu) micochondrion
(SGC3)
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08-UHI1995 #sequence_revision 21-UHI-1995 #text_change
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Meder Chic Communettic variable surface
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$65585 *type complete probable NAUPy-dependent oxidoreductase StrU - Streptomyces glaucesens *formal_name Streptomyces glaucesens 12-Mar-1996 secquence_revision 11-Mar-1997 stext_change 09-Sep-1997.
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**Authors**
**Authors**
**Bayer, 5.: Distier, J.: Pieperaberg, W.
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\$200 6.0. 1431 1 DAPK_STOAM DEATH ASSOCIATED PROTE 2.58+02 221 6.0. 1431 1 SUR_PARCS 222 6.0. 1431 1 SUR_PARCS 223 6.0. 1431 1 SUR_PARCS 223 6.0. 1432 1 SUR_PARCS 223 6.0. 1433 1 SUR_PARCS 223 6.0. 1434 1 SUR_PARCS 223 6.0 1434 1 SUR_PARCS 223 6 SUR_PA	Mon Dec 21 09:28:24 1998 US-08-951-733-14.zap	\$110 6 0.6 831 1 AL, MINA PROTEIN 4.1 (BAND 4.1) 2.58+02 \$120 6 0.6 835 1 CC48 (TMSST CELL DAVISION COMPRIOL 2.58+02 \$121 6 0.6 882 1 CC48 (TMSST CELL DAVISION COMPRIOL 2.58+02 \$122 6 0.6 882 1 CC48 (TMSST CALCADARY) TYPE 2.58+02 \$123 6 0.6 882 1 CC48 (TMSST CALCADARY) TYPE 2.58+02 \$124 6 0.6 882 1 CC48 (TMSST CALCADARY) TYPE 2.58+02 \$125 6 0.6 882 1 CC48 (TMSST CALCADARY) TYPE 2.58+02 \$126 6 0.6 882 1 CC48 (TMSST CALCADARY) TYPE 2.58+02 \$127 6 0.6 882 1 CC48 (TMSST CALCADARY) TYPE 2.58+02 \$128 6 0.6 882 1 CC48 (TMSST CALCADARY) TYPE 2.58+02 \$129 6 0.6 882 1 CC48 (TMSST CALCADARY) TYPE 2.58+02 \$120 6 0.6 882 1 CC48 (TMSST CALCADARY) TYPE 2.58+02 \$120 6 0.6 882 1 CC48 (TMSST CALCADARY) TYPE 2.58+02 \$121 6 0.6 882 1 CC48 (TMSST CALCADARY) TYPE 2.58+02 \$121 6 0.6 882 1 CC48 (TMSST CALCADARY) TYPE 2.58+02 \$121 6 0.6 882 1 CC48 (TMSST CALCADARY) TYPE 2.58+02 \$122 6 0.6 882 1 CC48 (TMSST CALCADARY) TYPE 2.58+02 \$123 6 0.6 882 1 CC48 (TMSST CALCADARY) TYPE 2.58+02 \$124 6 0.6 882 1 CC48 (TMSST CALCADARY) TYPE 2.58+02 \$125 6 0.6 882 1 CC48 (TMSST CALCADARY) TYPE 2.58+02 \$126 6 0.6 882 1 CC48 (TMSST CALCADARY) TYPE 2.58+02 \$127 6 0.6 882 1 CC48 (TMSST CALCADARY) TYPE 2.58+02 \$128 6 0.6 882 1 CC48 (TMSST CALCADARY) TYPE 2.58+02 \$129 6 0.6 882 1 CC48 (TMSST CALCADARY) TYPE 2.58+02 \$120 6 0.6 882 1 CC48 (TMSST CALCADARY) TYPE 2.58+02 \$120 6 0.6 882 1 CC48 (TMSST CALCADARY) TYPE 2.58+02 \$121 6 0.6 882 1 CC48 (TMSST CALCADARY) TYPE 2.58+02 \$122 6 0.6 882 1 CC48 (TMSST CALCADARY) TYPE 2.58+02 \$12 6 0.6 882 1 CC48 (TMSST CALCADARY) TYPE 2.58+02 \$12 6 0.6 882 1 CC48 (TMSST CALCADARY) TYPE 2.58+02 \$12 6 0.6 882 1 CC48 (TMSST CALCADARY) TYPE 2.58+02 \$12 6 0.6 882 1 CC48 (TMSST CALCADARY) TYPE 2.58+02 \$12 6 0.6 882 1 CC48 (TMSST CALCADARY) TYPE 2.58+02 \$12 6 0.6 882 1 CC48 (TMSST CALCADARY) TYPE 2.58+02 \$12 6 0.6 882 1 CC48 (TMSST CALCADARY) TYPE 2.58+02 \$12 6 0.6 882 1 CC48 (TMSST CALCADARY) TYPE 2.58+02 \$12 6 0.6 882 1 CC48 (TMSST CALCADARY) TYPE 2.58+02 \$12 6 0.6 882 1 CC48 (TMSST CALCADARY)	Mon Dec 21 09:28:24 1998 US-08-951-733-14.zep
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ZZI REVISIONS. SAGA Y., TUNC J.-S., SHEN F.-W., BOYSE E.A.; PROC. NATL. ACAD. SCI. U.S.A. 84:1991-1991(1987). [3]

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REDLINE: 67000763.
REDLINE: 70000763.
REDLINE: 70000763.
REDLINE: RESULATOR CHAINS REDLINE REMBRAKE ASSOCIATION PROFINED THE CHAINS.
REDLINE: RESULATOR FOR CATALITIC CHAINS. ACTIVATION BY CAMP PRODUCES FOR ACTIVATION BY CAMP PRODUCES.
REDLINE: REDLI
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DOGOD;

O1.-JAN-1988 (REL. 06, GERATED)

O1.-JAN-1988 (REL. 06, GERATED)

O1.-HOW-1999 (REL. 05, LAST SECURACE UPDATE)

O1.-HOW-1999 (REL. 05, LAST ANTECTATION UPDATE)

LYPHROCITE COMPONEN AUTICEN LT-5 PRECURSOR (EC 3.1.3.48) (200 ED 150DPSM) (CD45) (T200).

TOPONEN (CD45) (T200).

TOPONEN (CD45) (MOUSE).

UPLANE (TARANCOLUS (MOUSE).

UPLANE (TARANCOLUS (MOUSE).

UPLANE (TARANCOLUS (MOUSE).
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119 LAPGFALLD 127
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SEQUENCE PROM N.A.
MEDILINE; 8631366.
SACA Y., TUNG J.-S., SHEN F.-W., BOYSE E.A.;
PROC. NATL. ACAD. SCI. U.S.A. 83:6940-6944(1986).
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(REL. 05, LAST SEQUENCE UPDATE)
(REL. 33, LAST ANNORATION UPDATE)
ENT PROTEIN KINASE TYPE II-ALPHA REGULATORY
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Pred. No. 1.50e-04;
0; Mismatches 0; Indels
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                    RP SEQUENCE OF 832-1152 FROM N.A.

RP SEQUENCE OF 832-1152 FROM N.A.

RE KEDLINE; 87092355.

RA MASCHEM PG.

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Best Local Similarity 100.0%;
Matches 8; Conservative
REDURES 6500657.

MEDLINE: 6500657.

DAVISON A.J., SCOTT J.E.;

J. GEN. VIRGOL. 67:1759-1816(1986).

J. GEN. VIRGOL. 67:1759-1816(1986).

1. FUNCTION. EXCLESS URACIL RESIDUES FROM THE DRA. WRICH CAN ARISE

1. FUNCTION. EXCLESS TOWACIL RESIDUES FROM THE DRA. WRICH CAN ARISE

ADALYMENASE OR DUE TO DEMINIATION OF CITOSINE.

1. SULLARITY BELONGS TO THE URACIL-DRA GLYCOSTIASE FAMILY.

PERI, 27715; DAMESS P.

PROSITE; PS00110; U_DRA_GLYCOSTIASE; 1.
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TISSUENT-FOELL;
HEDLINE, 8604565.
SHEN P.-W., SAGA Y., LITMAN G., FREEMAN G., TUNG
BOYSE E.A.;
PROC. MATL. ACAD. SCI. U.S.A. 82:7360-7363(1985).
[4]
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461 EEEDTDPR 468
                                                                                                                                                                                                                                                                                                                                                                                                                                 VARICELLA-SOSTER VIRUS (STRAIN DUMAS) (VSV).
VIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE; ALPHAHERPESVIRINAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-1989 (REL. 10, CREATED)
01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
15-UTL-1989 (REL. 36, LAST ANOTATION UPDATE)
UNACIL-DNA GLYCOSYLASE (EC 3.2.2.-) (UDG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 8; DB 1; Length 155;
Pred. No. 3.48e-02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           305 AA
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US-08-951-733-14.rsp

Query Match 0.8%; Score 8; DB 1; Length 305; Best Local Similarity 100 0%; Pred. No. 3.48e-02; Matches 8; Conservative 0; Mismatches 0; Indels

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DNA REPAIR: HTDBOLASE; GEVCOSIDASE, ACT_SITE 148 148 ENERAL BASE (BY SIMILARITY) SEQUENCE 305 AA: 34376 MM; DDD3564F CRC32;

Page 25

Mon Dec 21 09:28:24 1998

STANDARD;

PRT; 00

US-08-951-733-14.rsp

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BÉDUERCE DY 1-95 FROM N.A.

REPOLITE 3137082.

REPOSE E B. 950-LERGE R., SITARD J., MYKLEBUST F., BANSSON V.,

RA MANSEN T. TAKKEN K.

BLOCHIM, BIDPHYS, ACTA, 1350:89-1-06(1997).

RE BICCHIM, BIDPHYS, ACTA, 1350:89-1-06(1997).

CC 1- FUNCTION: TIPE IL REGULANCE CHAISS, MELITATE REMERANE ASSOCIATION

OF M BINDING TO ANCHORING PROTEINS, INCLIDING THE MAPZ KINASE.

CC 1- SUBURIT: THE INCRITYE PORM POP THE MENY SITE IS COMPOSED OF TWO

CC REGULANDRY CHAISS AND TWO CATALITIC CHAISS. ACTIVATION BY CAMP

PRODUCES TWO ACTIVE CANALYTIC MONORES AND A REGULATORY DIMER

CI TISSUES FROM FILTE CHAIN THESE OF REGULATORY CHAISS ARE FOUND:

CC 1-TISSUES FROM FILTE: FORM THESE OF REGULATORY CHAISS ARE FOUND:

CC 1-THE STROSPHORYLATED BY THE ACTIVATED CATALITIC CHAIN.

DR MENL: 394555; 2536481 .-.

DR FIRE: 301865; GARDIR.

DR SESS. POOLS. ANDRE.

DR SESS. POOLS. CANADRA.

RESS. 
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Best Local Similarity 100.0%;
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461 EZEDTDPR 468
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BINDING 343
SEQUENCE 400 AA;
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NP_BIND 69
BINDING 90
ACT_SITE 198 1
SEQUENCE 342 AA;
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372 LRPSLTGA 379
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105 RVLQRLCE 112
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PA1951; 01603; 13, CREATED)
01-JAN-1990 (REL. 13, LAST ENQUENCE UPDATE)
01-JAN-1990 (REL. 13, LAST ENQUENCE UPDATE)
15-JUL-1998 (REL. 16, LAST ANNOTATION UPDATE)
CAMP-DEPENDERT PROFIEM KINASE TYPE II-ALPHA REGULATORY CHAIN.
PRAMEALO ON PREA OR PRAMEA:
BUNGO SAPIEMS (HUTMAN): TORRONTA; VERTESNATA; TETRADODA; MAMMALIA;
EUTHERUTA; PHIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 89211413.
OYEN O., MYKLEBUST F., SCOTT J.D.,
FEBS LETT. 246:57-64(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE: PSO0107; PROTEIN KIMSE_ATP; 1.
PROSITE: PSO0108; PROTEIN KIMSE_ST; 1.
PROSITE: PSO0108; PROTEIN KIMSE_ST; 1.
PROSITE: PSO011 PROTEIN KIMSE_ST; 1.
PROSITE: PROTEIN KIMSE; ONCOGENE;
PROTEIN KIMSE;
PROTEIN K
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7. VIROL. 61:89-897(1997).
11- SIMILARITE MITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-
11- SIMILARITE MITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-
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77 A
90 A
198 B
198 B
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343 CU
44962 MW;
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AIP (BY SIMILARITY).
AIP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
MM; 1066243C CRC32;
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Pred. No. 3.48e-02;
0; Mismatches 0; Indels
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CAMP.
1F7A0D99 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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Best Local Similarity 100.0%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             HEST, YEAST STANDARD; PRT; 654 AA.

P13198.

10.-OCT.1996 (REL. 12, CREATED)

01-OCT.1996 (REL. 12, LAST ANDOTATION UDDATE)

01-OCT.1996 (REL. 14, LAST ANDOTATION UDDATE)

KITOCHOMBRIAL HART SHOCT PROTEIN SCIL PRECURSOR (ENDONUCLEASE SCEI OS DUBUNIT).

SSCI OR ENSI OR TURNOSSC CREATISINE (BRAKE & PALST).

DUARNOTH: SURVEY AND SCIL RESULTING PALST.

DUARNOTH: SURVEY AND SCIL RESULTING PALST.
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HEDLING, 875585

HEDLING, 875585

HEDLING, 875585

LOUISDISSEN, 56543-555(987)

LOUISDISSEN, 56543-555(987)

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LOUISDISSEN, 56543-555(987)

LOUISDISSEN, 5644-555(987)

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LOUISDISSEN, 5644-555

LOUISDISSEN,
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STRAIN-D373-10
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TISSUDE-HEART MUSCLE;
HEDLINE; 8222175.
TAKIO K., SKITH S.B., KREBS E.G., WALSH K.A., TITANI
PROC. MATL. ACAD. SCI. U.S.A. 78:2544-2548(1982).
PROC. MATL. ACAD. SCI. U.S.A. 78:2544-2548(1982).
     SEGUENCE FROM N.A., AND SEQUENCE OF 24-41.
STRAIN-IAM 4274;
MEDLINE: 90368701.
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| | | | | | | | |
461 EEEDTDPR 468
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II-JUI-1986 (REL. 01. LAST ENDURNCE UPDATE)
II-TEI-1986 (REL. 33. LAST ANNOTATION UPDATE)
CAMP-DEPENDENT PROTZIM KINASE TYPE II-ALPHA REGILATORY CHAIN.
REKARAA.
BOS TAURUS (BOVIIE). CHORDATA; VERTEBRATA; TETRAPODA; KAMMALIA;
EUTHREKA: ARTIONACTILA.
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CNMP_BINDING_2: 2.
CNMP_BINDING_3: 2.
CNMP_BINDING_3: DUPLICATION;
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PROSPRORUATION (BY SIMILARITY).
CAMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 8; DB 1; Length 403;
Pred. No. 3.48e-02;
0; Kismatches 0; Indels
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MORISHIMA N., NAKAGAWA K., YAMAMOTO E., SHIBATA T.; 13. BIOL. CHEM. 265:15189-15197(1990).

ENGUENCE PROM N.A. TRAIN-5286; ERDLINE; 9139759; ULMG M.-B. CHUNT J.-C., GALIBERT F.; PAST 11:775-781(1995).

FIRAL MANY NATIONAL MATRIX. DETECTED ALSO IN THE STRONG STRONG LOATION, HATOCHONDRIAL MATRIX. DETECTED ALSO IN THE STRUCK FIRE HEAT. SHOOT BE HEAT SHOCK PROTEIN 70 FAMILY, STRONGEST SHILLARITY HITMEN MITTOCHONDRIAL HEPFO AND WITH EACTERIAL DMAK.

DOG: MATCHES COTTONS SHEET MITOCHONDRIAL HEPFO AND WITH EACTERIAL DMAK.

DOG: MATCHES COTTONS SHEET MITOCHONDRIAL HEPFO AND WITH EACTERIAL DMAK.

DOG: MATCHES COTTONS SHEET MITOCHONDRIAL HEPFO AND WITH EACTERIAL DMAK.

BUSING LASSAS COLUSTOL:
DEB. LASSAS COLUSTOL:
BUSING LASSAS COLUSTOL:
DIR. NASAS: DPAGES. HEBTESI.

WESD: 191010, MATR.

MESSP: P19110, MATR.

MESSP: P19110, MATR.

MESSP: P19110, MATR.

MESSP: P19110, MATR.

SECURNE OF 24-18.

KEDLINE: 9109225.

SCHERER P. E., KRIZG U.C., HPANG S.T., VZSTWEBER D., SCHATZ G.,

ZHEO J. 9:415:4422(199).

PROFITOR: 65C1 IS AN ESSENTIAL MITOCHONDRIAL PROFEIR, IT

IN PARA ROLE IN SCHLITATING THE ASSENSIV OF SOME PROFEIR

ANY PARA ROLE IN SCHLITATING THE ASSENSIV FE THE MITOCHONDRIA. IT MAY IMITIZE THE EMERING

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SGD: L0000561: SSC1.

PROSITE: PS00297; HSP70_1: 1.

PROSITE: PS01029; HSP70_2: 1.

PROSITE: PS01029; HSP70_3: 1.

HEAT SHOCK, ATTP-SINDING; MUTIGENE PAMILY; MITOCHONDRION;
TRANSIT PEPTIDE: 23

MITOCHONDRION
TRANSIT PEPTIDE: 23

MITOCHONDRION
TRANSIT 24

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HEAT SHOCK PROTEIN **C**1

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ID PAN1_YEAST
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                                                 Query Match 0.8%;
Best Local Similarity 100.0%;
Matches 8; Conservative
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|||||||||
238 LPAPGARR 245
1222 AAVTPAAG 1229
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001965; 015684; 256 (REL_26, CREATED)
01-UL-1993 (REL_26, LAST SEQUENCE UPDATE)
15-UL-1994 (REL_36, LAST ANDOTATION UPDATE)
LOWE'S OCCLC-EREROREMAL SYNDROME PROTEIN.
CCEL.
BOND SAPIEMS (HUMAN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONPLICT 660 660 G -> E (IN REF. 2).
SEQUENCE 968 AA; 111485 MW; 53CE3BE2 CRC32;
                                                                                                                                                                 SEQUENCE 1480 AA;
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MISTRY S.;
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EURANYOTA; METAIOA; CHONDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUPAKUBERA
TISSUPAKUBER,
MEDILHE, 92334430.
ATTREE O, OLVES I.M., OKABE I., BAILEY L.C., NELSON D.L.,
LEWIS R.A., MITHEE R.R., NUSSBAUM R.L.,
MATURE 358:138-447(1921).
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Pred. No. 3.48e-02;
0; Mismatches 0; Indels
                                                 Score 8; DB 1; Leng
Pred. No. 3.48e-02;
0; Mismatches 0;
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                                                     Indels
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595 LKELVARV 602 ||||||| 99 LKELVARV 106

Query Match 0.8%; Best Local Similarity 100.0%; Matches 8; Conservative

Score 8; DB 1; Length 654; Pred. No. 3.48e-02; 0; Mismatches 0; Indels

္ပ Sdwg 0 634 643 650

HITOCHONDRION
HEAT SHOCK PROTEIN SSC1.
ASW-RICH.
ASW-RICH.
N > NN (IN REF. 2).
N -> D (IN REF. 2).
M -> D CEB31F62 CRC32;

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STRAINESSEC, JAST?;
STRAINESSEC, JAST?;
BARRELL B. G. BALOCCE, BANKIER A.T., BOWAN S., BROWN D.,
CURRELLER C., BANKIER R., COPSET T., DEAR S., DETLIN K., FRASER A.,
CURRELLER C., HAMLIN NI., BONSMELL T.S., BUNF S., JACELS K., CONES M.,
LOUIS E., MACHIN NI., BONSMELL T.S., DETLI C., PARSON D.,
DOILS E., MACHINESSEC, BOULE T., ODELL C., PARSON D.,
MACHINESSEC, BROWN M., TERLES C., BOWLET M., SELECTON J., SHITTH V.,
MACHINESSEC, SECTION SELECTION OF THE MACHINESSEC S.,
SUBMITED D. DOIL T. 1991 TO ENDL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         973521;
01-071-1993 (REL. 27, CREATED)
01-071-1993 (REL. 13, LAST SEQUENCE UPDATE)
01-NOW-1997 (REL. 35, LAST ANNOTATION UPDATE)
PART PROTEIN:
PART AND OR MDP3 OR YIRODGC OR YIBGC.
PART OR MTP3 OR MDP3 OR YIRODGC OR YIBGC.
PART OR WIFT OR MDP3 OR YIRODGC OR YIBGC.
PART OR WIFT OR MDP3 OR YIRODGC OR YIBGC.
PART OR WIFT OR WDP3 OR YIRODGC OR YIBGC.
PART OR WIFT OR WDP3 OR YIRODGC OR YIBGC.
PART OR WDP3 OR YIBGC.
PAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCHS A.B., DEARDORFF J.A.;
ELL 70:961-973(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND SEQUENCE OF 320-344; 352-375 AND 899-906.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AES J., TEODORU C., VALENCIA A., SENSEN C., WIEMANN S.,
IMMERIANN J., SANDER C., ANSORGE W.;
   15 X 12 AA APPROXIMATE REPEATS.
1-1.
1-2.
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1-7.
                                                                                                                                                                                                                                                                                                                                                                                                                                   BE A SUBUNIT
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Mon
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TD MINE ACC P09541;

DT 01-MAR-1998 ()

DT 01-PEB-1991 ()

DT 01-PEB-1996 ()

DT 01-PEB-1996 ()

DT MYOSIN LIGHT ()
                                                                                                                                                REFFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
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NE MEDILIE: 92109718

NE COLEDAN M. E. PAN Y. C. E., ETHERTON T. D.;

NE COLEDAN M. E., PAN Y. C. C., PETHERTON T. D.;

NE DECCHEM, BIOCHTER, RES. CONSUM. 181:1111-1116(1991).

NEL BECCHEM, BIOCHTER, RES. CONSUM. 181:1111-1116(1991).

NEL BECCHEM, BIOCHTER, RES. CONSUM. 181:1110 STIPMILATE THE GROWTH PROMOTING EFFECTS OF THE IGFS ON CELL CHICURE. THEY ALIZE THE COMPH.

C. INTERNATION OF JOES WITH THERE CELL SURPACE RECEPTORS.

C. SINIGATITY BELIANS 1GF-1.

C. SINIGATITY BELIANS TO THE INSULIN-LIKE GROWTH FACTOR BINDING DECENTIAL SURPACE SECTION OF SECT
                                                                                                                                                                                                                                                                                                                                                                                                                            8
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IBPZ_FIG STANDARD: PRT: 23 AA.

C PA483;

T 01-MAR-1992 (REL. 21 CREATED)

T 01-MAR-1992 (REL. 21 LAST SEQUENCE UPDATE)

T 01-FBS-1996 (REL. 31 LAST ANDOTATION UPDATE)

E INSULTH-LIKE GROWTH EATON HINDING PROTEIN 2 (IGE (IGE)—BINDING PROTEIN 2) (FRAGMENT).

SUS SCROPA (PIG).
                                                                        Query Match
0.7%;
Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                    PIR: A02016: RWHUTA.

HSSP: PO1607: HHIL.

T-CELL: RECEPTOR GLICOPPOTEIN: SIGNAL.

SIGNAL 28 139 T-CELL RECEPT

COMAIN 28 139 T-CELL RECEPT

COMAIN 111 135 D SEGMENT.

COMAIN 151 135 D SEGMENT.

COMAIN 151 135 D SEGMENT.

COMMIN 151 139 J SEGMENT.

DISCUENT 19 116

FON TER 119 119

SECUENCE 139 AA: 15441 MM; SEAE2341 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Opery Match 0.7%; Score 7: DB 1: Length 23; Best Local Similarity 10: 0%; Pred. No. 4.76+00; Matches 7: Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         21 09:28:24 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUS SCROFA (PIG).
EUNARYOTA, METASOA: CHORDATA; VERTESRATA; TETRAPODA; MAMMALIA;
EUTHERIA; ARTIODACTIA.
[1]
4 LLGASVL 10
||||||||
697 LLGASVL 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 RPPPAAP 21
|||||||
| 85 RPPPAAP 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               439 AAVTPAAG 446
                                                                                                             (REL. 10, CREATED)

(REL. 17, LAST SEQUENCE UPDATE)

(REL. 33, LAST ANNOTATION UPDATE)

T CHAIN 1, SLOW-TWITCH MUSCLE B/VENTRICULAR ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                     Score 7; DB 1; Length 139;
Pred. No. 4.47e+00;
0; Mismatches 0; Indels
                                                                                                                                                                                                                        T-CELL RECEPTOR ALPHA CHAIN V REGION V SECHENT.
D SECHENT.
J SECHENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                8EAE2341 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 AA.
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                                                                        0
                                                                        Gaps
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M
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                                                                                                                                                58 LRPSLTG 64
||||||||
372 LRPSLTG 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 AAPEPER 39
|||||||
264 AAPEPER 270
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MTL3 OR MCLIV.
MUS MUSCULUS (MOGS).
EUTHERIA: RODENTIA.
EUTHERIA: RODENTIA.
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TETRAPODA;

MANOMALIA;

US-08-951-733-14.rsp

Page 34

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TESTUT 12

TPA_EPRONS STANDARD; PRT: 139 AA.

AC PO4437;
DT 13-AGC-1987 (REL. 05, CREATED)
DT 13-AGC-1987 (REL. 05, CREATED)
DT 13-AGC-1987 (REL. 05, CREATED)
DT 7-CELL RECEPTOR ALPHA CHAIN PRECURSOR V REGION (CTL-L17).

DE 7-CELL RECEPTOR ALPHA CHAIN PRECURSOR V REGION (CTL-L17).

DE 7-CELL RECEPTOR ALPHA CHAIN PRECURSOR V REGION (CTL-L17).

DE 7-CELL SECRETOR ALPHA CHAIN PRECURSOR V REGION (CTL-L17).

DE 7-CELL SECRETOR ALPHA CHAIN PRECURSOR V REGION (CTL-L17).

DE 21ANTUTA. METAMONA. CHORDATA: VERTERATA: TETRAPODA; MAMMALIA;
DE 21ANTUTA. PRIMATES.

RE 11.

LIMITOROCENETICS 74:17-21(1986).

RE 1.

LIMITOROCENETICS 74:17-21(1986).

RE 1.

LIMITOROCENETICS 74:17-21(1986).

RE 1.

LIMITOROCENETICS 74:17-21(1986).

RE 1.

LIMITOROCENETICS 74:17-21(1986).
                                                                                                                                                                         RESULT 14

ID TOLLAMOUT STANDARD: PRI: 153 AA.

AC 010330:1956 (REL. 14, CREATED)

DI 01-007-1956 (REL. 14, LAST SOUTENCE UPDATE)

MYCONACTERION TUDERCULOSIS

OC PROMATYOTA, FIRMICUTES; ACTINOMYCETALES: MYCONACTERION N.

RE SOUTENCE PROM N.

AN OLIVER N. HARRIS D. BARRELL B.G., BALANDREAM N.

RE SUBMITTED (APR-1996) TO ENGL/GENARY/DOBY DATA BI

CC -1- SHILLANIT RELONGS TO THE AIPC/TSA FAMILY.

DR MEDI: 2706371 E235109: -

NE MYCOTENTICAL PROCESSIN

SOUTENCE 153 AA: 16819 MH; OPDIOCPC CRC13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 0.7%;
Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 0.7%;
Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR: S0280; S30280.

PROSITE: PS01117; ETH_MARR_FAMILY; 1.

TANSCRIPTION REGULATION: REPRESSOR: DNA-BINDING.

BEQUENCE 148 AA; 17255 MN; N4EONAE6 CRC32;
                                                                                                                                                                         STOURICE FROM N.A.

STRAIN-BJ7NY;

DLYER K., BARRIS D., BARRELL B.G., RAJANDREAM
GURNITED (APR-1996) TO ENGLYCERBAKK, DUBJ DATA
-1- SIMILARITE BELONGS TO THE AHRC/TSA FAMILY.
ENGL; 270692; 2833309;

SEQUENCE 133 AA: 16819 NH; OFDJOCFC CRC32;
27 RGAKNYL 33
|||||||
113 RGAKNYL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SECURNCE FROM H. A.

KEDLINE: 68736770

LEZIDEN J. K., FRANCER J. D., STRONINGER J. L.;

LEGIDEN J. K., FRANCER J. D., STRONINGER J. L.;

LEGIDEN J. K., FRANCER J. D., STRONINGER J. L.;

EMBL. 1111 1211-1214-760-7

EMBL. M1565; G138765; -.
                                                                                                                                                                                                                                                                                                                                                                                            YTCOBACTERIUM TUBERCULOSIS.
ROKARYOTA; FIRMICUTES; ACTINOMYCETALES; MYCOBACTERIACEAE
                                                                                        Score 7; DB 1; Length 153;
Pred. No. 4.47e+00;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 7: DB 1: Length 148;
Pred. No. 4.47e+00;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 7; DB 1; Length 51;
Pred. No. 4.47e+00;
O; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-951-733-14.rsp
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Page 36

SEQUENCE FROM N.A.
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AC P7.
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RISB_MCCTU STANDARD; PRT; 154 AA.
P71655; 10
10.140V-1997 (REL. 35, CREATED)
10.140V-1997 (REL. 35, LAST ANNOTATION DPDATE)
10.140V-1997 (REL. 31, LAST ANNOTATION DEPTANSE BETA CHAIN).

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SEQUENCE FROM N.A. STRAIN-H37RV:

RIBH OR MTCY2184.34. MYCOBACTERIUM TUBERCULOSIS. PRINARYOTA; FIRMICUTES; ACTINOMYCETALES; US-08-951-733-14.rsp

MYCOBACTERIACEAE

Page 37

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S # # # B

-1- SHILARITY: BELONGS TO THE 87P FAMILY OF REDGOMAL PROTEINS.

BOLL, LO7932, CA70152:
-PROSITE: PS00052; BEDGGMAL_97; 1.
REDGOMAL PROTEIN, CELEDROMAL_97; 1.
SEQUENCE 155 AA; 17769 MY; 6956CJAB CBC32;

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U8-08-951-733-14.xsp

Page 38

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ID MLETY_BAT STANDARD; PRT; 199 AA.
AC 916409; AC 916409; PRT; 199 AC 916409; PRT; 190 AC 916409; PRT; 190 AC 916409; PRT; 190 (REL. 15, LAST SECRETED)
DT 01-ARG-1990 (REL. 15, LAST SECRETATION UPDATE)
DT 01-FRE-1996 (REL. 13, LAST SECRETATION UPDATE)
ARTHUS MACHINETACON (BATT)
CC EUTHERIA; RODERTIA. CHORDATA; VERTEBRATA; TETRAPODA; MARGALIA;
CC EUTHERIA; RODERTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
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Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%;
Matches 7; Conservative
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856 GSILSTL 862
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P27474;
01-AUG-1992
01-AUG-1992
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RRI_SPIAX STANDARD: PRT: 155 AA.

PAJ342:
01-MOV-1995 (REL. 32, CREATED)
01-MOV-1995 (REL. 32, LAST REQUENCE UPDATE)
01-POV-1996 (REL. 31, LAST REQUENCE UPDATE)
01-POV-1996 (REL. 31, LAST ANNOVATION UPDATE)
REGARDIAST 305 RIBOSOMAL PROTEIN 67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 ALLDGAR 34
|||||||
124 ALLDGAR 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01 NOT 1992 (REL. 23. CREATED)
01 NOT 1992 (REL. 23. CREATED)
01 UT 1993 (REL. 25. AST ENGUENCE UPDATE)
10 DE POLITICO DE PLANTAMENTO DE PLAN
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CONJUGATOPHYCEAE; EYGNEMATALES; EYGNEMATINEAE; EYGNEMATACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPIROGYRA MAXIMA.
CHLOROPLAST.
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242 GARREGG 248
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EW K.A., MANHART J.R.;
PHYCOL. 29:500-505(1993).
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Pred. No. 4.47e+00;
0; Mismatches 0; Indels
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Pred. No. 4.47e+00;
0; Mismatches 0; Indels
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REPORTED FROM N.A.

RESTRICTION NO.

RESTRICTION NO
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Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%; Pred. No. 4.47e+00;
Matches 7; Conservative 0; Mismatches 0; Indels
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                                                                                                     29 AAPEPER 35
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264 AAPEPER 270
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RUYC_PSAR STANDARD; PRT; 174 AA.

Q51424; G1424; G
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||||||||
243 ARRRGGS 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-WISTAR, TISSUE-HEART VENTRICLE;
MEDLINE; 90016857.
PERIASANY M., WODGAONKAR R., KUMAR C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECURNCE PROM N.A.
TISSUE-HEART VENTICLE;
HEDLINE: 89240011.
HCHALLY E., BUTTRICK P., LEINWAND L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           164 GARREGG 170
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PROMARIOTA, GRACILICUTES: SCOTOBACTERIA; AEROBIC RODS AND COCCI;
PSEUDOMORADACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               199 AA; 22025 MW; 0426BB63 CRC32;
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Pred. No. 4.47e+00;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 7; DB 1; Length 199;
Pred. No. 4.47e+00;
0; Mismatches 0; Indels
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VARSPLIC 164
VARIANT 62
VARIANT 202
SEQUENCE 261 AA;

194 M 62 G 202 P 28385 MW;

MISSING (IN EARLY ELA 24 KI G -> E (IN STRAIN GRIDER). P -> G (IN STRAIN GRIDER). 4; P262C2BA CRC32;

KD PROTEIN)

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Matches
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PATE TRACE
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STRAIN-COMEN;
MEDIJUR; B1237792.
MEDIJUR; B1237792.
DJURSA, R., DEXKER B.H.M., V
BOYER H.W.;
BOYER H.W.;
CENE 12:287-299(1980).
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MIM: 27460: TRANSPORT: DISEASE MITATION.

TRANSPORT: DISEASE MITATION.

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TORRILOT 271 771 5 -> R (IN REF. 2).

SEQUEENCE 278 AA; 31749 MM; B3827397 CRC32;
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SAME PRIMARY TRANSCRIPT FROM THE ELA REGION OF THE GENOME.

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H_FING 163 183 C4-TIPE.
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810 DAVVIEQ 36
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230 REAGVPL 236
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MAGGENGON S.;

SUBMITTED (MOY-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.

III SIMILARITY: TO RUMAN PROTEIN D52.

EMBL: 568105; G1072144;

WORNTEN; F5155.1: CE03198.

SEDQUENCE 257 AA; 28696 NM; 66FDB900 CRC32;
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TUMOR RES. 19:94-47(1984).
-1- FUNCTION: TRANS-ACTIVATES BARLY VIRAL PROMOTERS AND SOME CELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRAIN-GRIDER;
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LERBANDER P. E., ANDERSEN R. N., CANESHUDAR N.;
SECT. LINUN. 52:4459-4450(1994).
- SUCCELLULAR, LOCATION: LYTECRAL MEMBRANE PROTEIN (PROBBLE).
- SIMILARITI: BELONGS TO THE AGC-3 SUPPRAKIN OF INTEGRAL MEMBRANE
- SIMILARITI: BELONGS TO THE AGC-3 SUPPRAKIN OF INTEGRAL MEMBRANE
                                          h 0.7%; Score 7; DB 1; Length 278; Similarity 100.0%; Pred. No. 4.47e+00; 7; Conservative 0; Nismatches 0; Indels
                                                                                                                                                                           7; G310632; ...
NE: TRANSPORT.
18 TRANSPORT.
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278 AA: 2970;
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DESCRIPT 22

DESCRIPTIONAN STANDARD: PRI; 278 AA.

AC DISSULTA 1996 (REL. 33 CHEATED)

DT 01-FED-1996 (REL. 31 LAST SEQUENCE UPDATE)

DE ALPHA-TOCOPHEROL TRANSFER PROTEIN (ALPHA-TIP).

DE POALPHA-TOCOPHEROL TRANSFER PROTEIN (ALPHA-TIP).

DE POALPHA-TOCOPHEROL TRANSFER PROTEIN (ALPHA-TIP).

RE SEQUENCE PROM N.A.

RE MEDILIES 9516418

RATHAL N. SATOL MIYATA A., TANABE T., TANABASHI A. MANTHA H., SATOL MIYATA A., TANABE T., TANABASHI A. MEDILIES 9516418

RA MANTHA H., SATOL MIYATA A., TANABE T., TANABASHI A. MANTHA H., SATOL MIYATA A., TANABE T., TANABASHI A. MEDILIES 9516418

RA MANTHA H., SATOL MIYATA A., TANABE T., TANABASHI A. DESGR H. A., LEPATAI A., SIDDIQUE T.;

RA MANTHA H., SATOL MIYATA A., TANABE T., TOKOTA T., AR MEDILIES 9505448.

RA MANTHA H., SATOL MIYATA A., TANABE T., TOKOTA T., AR MANTHA H., SATOL MIYATA H., TANABASHI A., SEDELLULAR MEDISANZES.

CC 1- SEPLANTE MEDISAN
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RESULT 25
ID SAPB_SALTY STANDARD; PRT: 321 AA
ID SACES:
DT 01_UN-1994 (REL. 29, CREATED)
DT 01_UN-1994 (REL. 29, LAST SEQUENCE UPDATE)
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RE SECURACE FROM N.A.

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1 01-80V-1997 (REL. 35, CREATED)

1 01-80V-1997 (REL. 35, LAST SEQUENCE UPDATE)

1 01-80V-1997 (REL. 35, LAST ARROTATION UPDATE)

2 DAM_FROZIERS

2 DAM_FROZIERS

3 STRECHOCTERS OF LICTURES OXFPHOTOBECTERS

4 CTANDBACTERS ON DESCRIPTION OF CREATE

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Best Local Similarity 100.0%;
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Best Local Similarity 100.0%;
Matches 7; Conservative
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VARANT AVED GLM-101.

VARANT NES $6016648.

GOTODA T., RITTA M., ARAI H., INGUE K., YORGTA T., FUNDO Y.,

VARANT Y., YAMADA N.;

HAM T. YAMADA N.;

HEW ENGL. J. HED. 3331311-1318 (1995).

HE WENGL. J. HE WENGL. 
                                                                                                                                                                                                                                                                             129 VVSPARP 135
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294 VVSPARP 300
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862 LLCSLCY 868
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699 GASVLGL 705
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UMARTOVA: METALON: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
UÇTERATA: PATRATES.
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ENG H.X., HENTATI A., SIDDIQUE T.;
ENBHITTED (FEB-1995) TO EMBH/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 7; DB 1; Length 307;
Pred. No. 4.47e+00;
0; Mismatches 0; Indels
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Pred. No. 4.47e+00;
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                                                                                                                    321 AA
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RESULT 16

ID SAPE POOLI STANDARD: PRT: 321 AA.
AC 047523; P7689;
D7 01-WOY-1997 (REL. 35, CREATED)
D7 01-WOY-1997 (REL. 35, LAST SEQUENCE UPDATE)
D7 01-WOY-1997 (REL. 35, LAST SEQUENCE UPDATE)
D7 01-WOY-1997 (REL. 35, LAST SEQUENCE UPDATE)
D8 PEPTIDE TANSPORT STSTEM PENHEASE PROTEIN SAPB.
G8 SECHERICHA COLI.
C6 PROMANTOAL GRACILICOUTES; SCOTOBACTERIA: PACULTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mon
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Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%;
Matches 7; Conservative
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09704 1945 (REL. 22, CREATED)

01-007 1945 (REL. 23, CREATED)

10-007 1945 (REL. 23, LAST SCOURMCE UPDATE)

10-007 1945 (REL. 33, LAST ANOTATION UPDATE)

10-007 1945 (REL. 33, LAST SCOURME LOSSION TEAST).
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010314;
01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-WOT-1999 (REL. 35, LAST SEQUENCE UPDATE)
01-WOT-1999 (REL. 35, LAST ANNOTATION UPDATE)
01-WOT-1999 (REL. 35, LAST ANNOTATION UPDATE)
01-WOT-1990 (REL. 34, CREATED)
01-WOT-1990 (REL. 35, CREATED)
01-WOT-1990 (REL. 35, CREATED)
01-WOT-1990 (REL 35, CREATED
SEQUENCE FROM M.A.
SEQUENCE FROM M.A.,
SERVIN 973; SURROCHER C.M., BARRELL B.G., BAJANDREAM M.A.,
SERVINE (FEEL-1988) TO EMELORE BROWN DEBT BARRS.
1. SERVINETT: BELONGS TO THE IUNH FAMILY.
BEST, 165795; SEZ23976;
BEST, 165795; SEZ23976;
BEST, 165795; SEZ23976;
BEST, 165795; SEZ23976;
BEST, 165795; SEZ39976;
BEST, 165796; SEZ39976;
BEST, 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       287 ASRSLPL 293
|||||||
250 ASRSLPL 256
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||||||||
|119 LAFGFAL 125
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STRAINE-1028S.
MEDLINE: 94036887.
MEDLINE: 1004710N: INFOGRAL MEDERANE PROTEIN: INFORMATION: INFOGRAL MEDERANE PROTEIN: INFORMATION: MEDERANE
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SEQUENCE 329 AA; 36687 MM; 863653FB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENDIEMCE FROM N.A.

STWAIN-972:
GEFILES G. CHURCHER C.M., BARRELL B.G., RAJANDREAM N.A., WALSE S.V.;
SUBMITTED (JUL-1993) TO ENGL/CENBANK/DDSD DATA BANKS.
SUBMITTED (JUL-1993) TO YEAST YEROGSC.

-- SINILARITY STRONG, TO YEAST YEROGSC.
EMBL: ESO143; G.005799; --
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EUKARYOTA: FUNGI: ASCONYCOTINA: HEMIASCOMYCETES.
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                                            01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
PEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN SAPB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESCHERICHIA COLI.
Prokartota; gracilicutes; scotobacteria; pacultatively anaerobic rods;
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BROKANYOTH. GRACILICUTES; SCOTOBACTERIA; PACULTATIVELY AMAEROBIC RODS;
SYTEROBACTERIACSAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN-DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE OPPEC
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819986 539586
819986 539586
7E: PSGO402: BP_TRANSP_INN_MEMBR, FALSE_MEG.
7E: PSGO402: BP_TRANSP_INN_MEMBR, FALSE_MEMBR, FALSE_ME
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Pred. No. 4.47e+00;
0; Mismatches 0; Indels
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Pred. No. 4.47e+00;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                               Page 45
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-2 PROFEIN-DEPARTAL
-2 SUBPARITY
-2 SUBPARIT
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              RESULT 30
ID EXAMPLE STANDARD; I
AC Q59083;
DT 01-NOV-1997 (REL. 35, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dec 21 09:28:24 1998
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C PA705;
C PA705;
T 01-FEB-1996 (REL. 3), CREATED)
T 01-FEB-1996 (REL. 3), LAST SEQUENCE UPDATE)
T 01-OCT-1996 (REL. 3), LAST SEQUENCE UPDATE)
E PETITO O ROTEIN.
N PETITO OR TATOGREY OR J1282.
N PETITO OR TUNGI; ASCONTOCTIAN; REMIASCONTCETES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.7%;
Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%;
Matches 7; Conservative
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472 QLIRQHS 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGUENCE FROM N.A.

POREL T.M., MALTRAYLE G.

FORELT M. SELINOYLE G.

FORELT M. SELINOYLE G.

FORELT M. R. ANG. ENOW, PET130 MUTANTS ARE DEFICIENT IN MITOCHONDRIAL

PROPERLY SEVENESIS.

-1. SUBCELLIAL LOCATION: MITOCHONDRIAL HATRIX (POTENTIAL).

ENGL. 107712; G1021819;

ENGL. 149296; G1060745;

ENGL. 149296; G1060745;

MITOCHONDRIAUM.

SEDULNO30025; PET130.

MITOCHONDRIAUM.

SEDULNO30025; ANG. 39812 MM; 85A89097F CRC12;
                                                                                                                                                                                                                                                                                                         67 STLTDLQ 73
|||||||
786 STLTDLQ 792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE 330 AA;
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|||||||
119 LAPGFAL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEDUENCE FROM N.A.
CUI E. MASON T.'
SUBMITTED (OCT-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENGIENCE PROM N.A.

TRAINERIZAMA T., POSTONA K., HAYASHI K., BONTO A., HORITCHI T.,

TEMATERIZAMA T., TOSTONA K., TEONO S., TONE T., KANAI K., ENAMI K., ENA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-RIZ, MG1855;
SUMMITTED (JAN-1997) TO EMDL/GENBANK,DOBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGUENCE FROM N.A.
STRAIN-KL12 / PRAGS;
PESTEIN W., NOELEER E., STUNDE S., TEWES R., SCHMID R., BAKKER E.P.;
DUNITTED (APR-1996) TO EMBL/GEHBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENTEROBACTERIACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-
PROTEIN-DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE OPPBC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36063 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 7; DB 1; Length 330;
Pred. No. 4.47e+00;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 7; DB 1; Length 321;
Pred. No. 4.47e+00;
0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 7; DB 1; Length 347;
Pred. No. 4.47e+00;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60ACC6BB CRC32;
                                                                                                                    348 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-951-733-14.rap
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JOSPIRILLON BRASILENSE.
ASANID MEGADIASHID P90.
NOKARTOTA, GRACILICUTES; SCOTOBACTERIA;
ROBIC, MOTILE, HELICAL AND/OR VIBRIOID.
                                                                                                                                                                      I-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
1-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
D-GLUCOSE 4-EPINERASE (EC 5.1.3.2) (UDP-GALACTOSE 4-EPINERASE)
ALACTONALDENASE).
```

SEQUENCE FROM N.A. STRAIN-SP7 / ATCC 29145;

342 GGSASRS 348 ||||||| 247 GGSASRS 253 Match 0.7%; Score 7; DB 1; Length 348; Local Similarity 100.0%; Pred. No. 4.47e+00; Endels 7; Conservative 0; Mismatches 0; Indels

> 0 Saps

8

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SEQUENCE FROM N.A.
TISSUE-PLACENTA;
MEDLINE; 94359483.
REGAN J.W., BAILEY T.J., PEPPERL D.J., PIERCE K.L., BOGARDUS A.M.

Kon 8 21 09:28:24

US-08-951-733-14.rs

IRRE JUMAN

OSPITA: (09146: OROSGA:
01:NOV-1997 (REL. 35, CREATED)

O1:NOV-1997 (REL. 35, CREATED)

O1:NOV-1997 (REL. 35, CREATED)

15-UUL-1998 (REL. 36, LAST REGUENCE UPDATE)
15-UUL-1998 (REL. 36, LAST REGUENCE UPDATE)
ATP-SENSITUR UNMARD RECTIFIERS OFFAILT J, MEMBER 15 (DOWNARD
RECTIFIERS OFFAILT S, SUSPAILT J, MEMBER 15) (INARD
RECTIFIERS OFFAILT S, RETAINS (REAL 3)

REMANOYN, METARNA CHONDATA: VENTEBRATA; TETRANDOA; MANGALIA;

UNIMERAL, FRANCES:

EQUENCE FROM N.A. ISSUE-KIDNEY:

OURNIE FROM N.A.
SSUP-KIDNEY:
UCK M.E. PISST T.M., BOCK J.H., SLIGHTOM J.L., LEE
ERROWSKI M.J.: 772:586-593(1997).

OHIRA M., SEKI N., NAGASE T., SUZUKI B., NOMURA N., OHARA O., HATTORI M., SAKAKI Y., EKI T., MUBAKAHI Y., SAITO T., ICHIKAWA BMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS

REPORTE PROME N.

REPORTE P. GERANA CA., KORN B., TASPO M.-L., POUTSKA A.,

RECURING 44:217-244(1997).

RECURROR SALES PORTER P. M., CREAU N. J.

RECURROR SALES PORTER P. M., CREAU N. J.

RECURROR SALES PROME P. M., CREAU N. J.

RECURROR SALES PROME P. M., CREAU N. J.

RECURROR SALES P. M., CREA

NNEL; ION TRANSPORT; TRANSPORT.

91 CYTOPLASMIC (POTENTIAL)
M1 (POTENTIAL).

Page

NO. Dec 21 09:28:24

US-08-951-733-14.rsp

DOMAIN TRANSMEM DOMAIN SITE 117 142 163 157 162 162 375 #\$ (PORE-PORMING) (POTENTIAL).

#2 (POTENTIAL)

ROLE IN THE CONTROL OF POLYMINE HEDIATED

CHANELL GATING AND IN THE BLOKING BY

INTRACELLIFIAN MONESIUM (BY SIMILARITY).

D > 0 (IN REF. 3).

V > A (IN REF. 2).

S = 0 (IN REF. 2).

CONFLICT CONFLICT CONFLICT SEQUENCE 98 235 245 375 AA; 235 245 42635 MW;

PEFFFFFF

Query Match 0.7%; Best Local Similarity 100.0%; Matches 7; Conservative Score 7; DB 1; Length 375; Pred. No. 4.47e+00; O; Mismatches 0; Indels . Gaps

0

260 ETSPLRD 266 |||||||| |004 ETSPLRD 810

17 13
GALLSTELL STRUARD: PRT; 397 AA.
P13277:
01-7AN-1990 (REL. 13, CREATED)
01-NOV-1995 (REL. 21, LAST SEQUENCE OPDATE)
01-NOV-1995 (REL. 32, LAST SEQUENCE OPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION OPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION OPDATE)

STREPTOMYCES LIVIDANS. PROKARIOTA: FIRMICUTES; ACTINOMYCETALES; STREPTOMYCETACEAE.

SEQUENCE PROM N.A.
MEDILHE; 88085669.
ADMHS C.M., FORWARLD J.A., SCHMIDT P.J., ROSENBERG M., BRAWKER M.E.;
J. BACTERIOL. 170:203-212(1988).

RP IDENTIFICATION OF PROBABLE FRAMESHIPTS.

RA CIBSON T.J.;

RA CIBSON T.J.;

RI UNPUBLISHED OBSERVATIONS (MAR-1995).

CC --- CANALTYIC ACTIVITY: ATP + D-GALACTOSE - ADP + D-GALACTOSE

CC --- PATRHAN: ETIST TEACTION OF GALACTOSE METABOLISM (LEIGH PATRHAY).

CC --- PATRHAN: ETIST TEACTION OF GALACTOSE METABOLISM (LEIGH PATRHAY).

CC --- CAUTION: REF. 1. SEQUENCE DIFFERS FROM THAT SHOWN IN POSITIONS 49

CT D 63, 181 TO 244, AND 288 TO 310 DE TO FAMESHIPTS.

CC TD 63, 181 TO 244, AND 288 TO 310 DE TO FAMESHIPTS.

CR PIR: C18663 KING.

C18663

Dec 21 09:28:24 1998

Page 49

US-08-951-733-14.rap

Page 50

DONELLO J.E., FAIRBAIRN C.E., KEDZIE K.M., WOODWARD D.F., GIL D.W.;

SUBSTITED (JAN-1995) TO ENGL/GERBANK/DDSJ DATA BANKS.

-1- PROWCTION: RECEPTOR FOR PROSTACLANDER 2 (PG22). THE ACTIVITY OF
THIS RECEPTOR IS MEDIATED BY G-S PROFERIS THAT STIMULATES
ADBITIATE CYCLASE. THE SUBSEQUENT BASES IN INTRACELLAR CAMP I
RESPONSIBLE FOR THE RELAXING EFFECT OF THIS RECEPTOR ON SHOOTH R CAMP IS

1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
1- TISSUE SPECIFICITY: PLACENTA AND LUNG.
1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED

G_PROTEIN_RECEPTOR: 1.
RECEPTOR: TRANSMEMBRANE: GLYCOPROTEIN
EXTRACELLULAR (POTENTIAL).

EMBL: 019487 (633850
EMBL: X838681 (633205)
EMBL: X838681 (633205)
EMBL: X838681 (632205)
EMB: X838681 (632205)
EMBL: X838681 (622205)
EM POTENTIAL.

POTENTIAL.

BY SIMILARITY

A -> R (IM REF. 2).

A -> R CRC32; EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL).
CTYOPLASHIC (POTENTIAL).

6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CTYOPLASHIC (POTENTIAL). MAR (POTENTIAL) (POTENTIAL). (POTENTIAL).

Query Match

Best Local Similarity 100.0%;
Matches 7; Conservative Score 7: DB 1: Length 358; Pred. No. 4.47e+00; 0; Mismatches 0; Indels Indels 0 Caps

245 PGARRRG 251 ||||||| 241 PGARRRG 247

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Mon Dec 21 09:28:24 1998
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Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.7%;
Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 0.7%; Score 7; DB 1; LA
Best Local Similarity 100.0%; Pred. No. 4.47e+00;
Matches 7; Conservative 0; Mismatches
                                                                                                                      OPAL_PSAKE STANDARD: PRT: 479 AA.
051397;
051397;
01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST ESQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ESQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ENGLATION UPDATE)
04-NOV-1997 (REL. 35, LAST ENGLATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       212 KRAERLT 218
|||||||
671 KRAERLT 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE: PS00543; HLYD_PAMILY: 1.
HEMOLYSIS: TRANSPORT: TRANSPERDRANE;
DOMAIN
1 1 0 0 0 POTENTIAL
DOMAIN 60 80 POTENTIAL
DOMAIN 91 478 PERFUAS
SEQUENCE 478 AA; 54591 NM; 721A00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YHHG, PEAST STANDARD: PRT; 465 AA.
P38845;
O1-F28-1995 (REL. 31, CREATED)
O1-F28-1995 (REL. 31, LAST SEQUENCE UPDATE)
O1-C77-1996 (REL. 31, LAST SEQUENCE UPDATE)
O1-C77-1996 (REL. 31, LAST SEQUENCE UPDATE)
O1-C77-1996 (REL. 31, LAST SEQUENCE UPDATE)
UPDATETICAL 51.1 ND PROTEIN IN DCD1-HEPD6 INTERGENIC REGION.
YELLIGH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 397 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (2)

TOPOLOGY.

TOPOLOGY.

SCHEMEZIN R., GERYSCHEV I., MOLLENKOPF H.-J., GOZZEL W.;

SCHEMEZIN R., GERYSCHEV I., MOLLENKOPF H.-J., GOZZEL W.;

SCHEMEZIN R. DOCATION THE TRANSPORT OF HEMOLISIN A.

STRUCTION: INVOLVED IN THE TRANSPORT OF HEMOLISIN A.

STRUCTION: INVOLVED IN THE TRANSPORT OF SCHEMICAL PROTEINS.

PROSITE JOSCHAFFILLED.

PROSITE: P
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DO E. PAYELLA A. PULYON L. GATTUNG S., GEISEL C., KIRSTEN J.,
DO E. PAYELLA A. PULYON L. GATTUNG S., GEISEL C., KIRSTEN J.,
GUCARN T., HILLIER L., JIER H., JOHNSTON L., LANGENON Y.,
LARREILLE P., LOUIS E.J., MACHI C., MADDIS E., MATSEES S., MOUSER L.,
MIRJA H., RIFKIN L., RILES L., ST PETER H., TREVASKIS E., VAGGHAN K.,
VIGNAII D., HILCON L., WOHLDMAN P., WATERSTON R., WILSON R.,
VIGNAII D., HILCON L., WOHLDMAN P., WATERSTON R., WILSON R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               377 PRRGAAP 383
|||||||
260 PRRGAAP 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
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PROMARYOTA: GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
ENTENOBACTERIACEAE.
     PSEUDOMONAS AERUGINOSA.
PROMARYOTA: GRACILICUTES: SCOTOBACTERIA: AEROBIC RODS AND COCCI:
PSEUDOMONDACEAE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=396 / SEROTYPE 04;
STRAIN=396 / SEROTYPE 04;
STEMINE; 85234404.
FELMINE T., PELLETT S., WELCH R.A.;
J. BACTERIOL. 163:94-105(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1-MAR-1999 (REL. 10, CREATED)
1-MAR-1999 (REL. 10, LAST SEQUENCE UPDATE)
1-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
REPOLISIN SECRETION PROTEIN D, CHROMOSOMAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCHAROMYCES CEREVISIAE (BAKER'S YEAST).
KARYOTA; FUNGI; ASCONYCOTINA; HEMIASCONYCETES
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Pred. No. 4.47e+00;
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GGESPSTSPRGGACWSSTFGASSTFJANSTASARALRE
ADTRIKAGNIVJEGRSILEDDERIGCPELLIVVDTALASAL
C -> ATGASANSSSMATFJARRIJPHLPAGPGRRIGGE
LECTR (1H REF. 1).
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POTENTIAL.

PERIPLASMIC (POTENTIAL).

721A007E CRC32;
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(IN REF. 1).
RGGHALPLDTRDLSGROIPPDLAAEGMTLLVVVVV
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SMIC (POTENTIAL)
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ID U121_19VIE

AC P09855;

AC P09855;

DT 01-MAR-1989 (R
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DE PENOTEIN U121:
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ID HLY4_ECOLI
AC P09986;
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X SCHUTLEN R. GENTS. 14:155-163(1992).

L MOL. GEN. GENTS. 14:155-163(1992).

C --- FUNCTION: INVOLVED IN THE FRANSPORT OF HEDUTSIN A.

C --- SUBCELLIAR INVOLVED IN THE FRANSPORT OF RECERTION.

C --- SINCLIARIY: BELONGS TO THE HUTD FAMILY OF SECRETION PROTEINS.

C --- SUBCLIARIY: BELONGS TO THE HUTD FAMILY OF SECRETION PROTEINS.

PIR: S100158.

M PIR: $10058; $10058.

M PERI: MINISTER S10058; TANSPORTS. INNER MEDGRAME; PLASHID.

M PERI: MINISTER S10058; TANSPORTS. THERE MEDGRAME; PLASHID.

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Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%;
Matches 7; Conservative
Query Match
                                                           SECORME FROM N.A.
MEDILINE: 6520155.
COMPELS U., MINSON A.
VINCLORY 133-132-0-247(1986).
-1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL21.
-1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL21.
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553 AAEHRLR 559
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671 KRAERLT 677
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P067739:
01.-JAN-1998 (REL. 05, CREATED)
01.-JAN-1998 (REL. 05, LAST SECURACE UPDATE)
01.-JAN-1998 (REL. 34, LAST ANNOWNICH UPDATE)
01.-OTT-1996 (REL. 34, LAST ANNOWNICH UPDATE)
HENGLYGIN SECRETION PROTEIN D, PLASMID.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN HYEM).
VIRIDAE: DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE; ALPHAHERPESVIRINAE
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ESCHERICHIA COLI.
PENASHID PHIX152.
PROKANCOTA. GRACLICUTES: SCOTOBACTERIA: FACULTATIVELY ANAEROBIC
ENTEROBACTERIACEAE.
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IESS J., WELS W., VOGEL M., GOEBEL W.;
PENS MICROBIOL. LETT. 34:1-11(1986).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (REL. 10, CREATED)
(REL. 10, LAST SEQUENCE UPDATE)
(REL. 24, LAST ANNOTATION UPDATE)
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0.7%; Score 7; DB 1; Length 535;
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Pred. No. 4.47e+00;
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Pred. No. 4.47e+00;
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Best Local Similarity 100.0%; Natches 7; Conservative 137 LRVRAQD 143 ||||||| 717 LRVRAQD 723 Pred. No. 4.47e+00; 0; Mismatches 0; Indels 0; Caps 0

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DE DUZALJEVII
AC P10305;
AC P10305;
DI O1-MAR-1999 (10 O1-MAR-1992 (10 DT O1-DE-1992 RPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17). RIDAE: DS-DNA ENVELOPED VIRUSES: HERPESVIRIDAE; (REL. 10, CREATED) (REL. 10, LAST SEQUENCE UPDATE) (REL. 24, LAST ANNOTATION UPDATE) STANDARD; PRT; 535 AA

ALPHAHERPESVIRINAE

SÉDURACE PROM N.A.

REMEDILIE: SESTABLE M.A. DAVISON A.J., DOLAN A., FRAME H.C.,

N. MCERCH D. PERROLL S. SCOTT . B., TANLOR P.,

LA MCHAND . DERIVALIT . BLONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL21,

C. SHILARITI . BLONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL21,

NO EDEL DION'S . ESTY-4 UL21, AND VEV 38.

REMEDIATED . DESTY-4 UL21, AND VEV 38.

REMEDIATED .

밁 Query Match 0.7%; Score 7; DB 1; Length 535; Best Local Similarity 100.0%; Pred. Mo. 4.47e+00; Matches 7; Conservative 0; Mismatches 0; Indels 137 LRVRAQD 143 ||||||| 717 LRVRAQD 723 Indels 0 Gaps

0

RESULT TO TAN DE TO 000 DE TO 0000 DE TO 000 D THE TRAST STANDARD; PRT: 546 AA.

1112 TAST
112 TAST
113 CHEALTE; PRT: 546 AA.

114 TAST 1999 (REL 18 LEFT SEQUENCE UPDATE)
11 FER-1996 (REL 18 LAST MINOZATION UPDATE)
11 FER-1996 (REL 18 LAST MINOZATION UPDATE)
12 TRAN NUCLEOTIVITANISTE MASE PRECURSOR (CC 2.7 7.7.25)
ADMYLLTIPANISTERASE) (TRAN CCA-PTROPROSPHORILASE).

CCAL OR TWILD ON TRAILSC.

CCAL OR TWILD ON TRAILSC.

CCAL OR TWILD ON TRAILSC.

Mon 90 21 09:28:24 1998

Best Local Similarity 100.0%; Matches 7; Conservative Pred. No. 4.47e+00; 0; Mismatches 0; ö Caps

STE_METTH STANDARD; PRT: 552 AA.

959343;
01.NOV-1997 (REL. 15, CREATED)
01.NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOVATION UPDATE)
16-JUL-1998 (REL. 36, LAST ANNOVATION UPDATE) URS).

THANOBACTERIUM THERMOAUTOTROPHICUM (STRAIN MARBURG / DSM 2133). CIAEBACTERIA, EURYARCHAEOTA; METHANOBACTERIALES;

ETHANOBACTERIACEAE

135 EDTDPRR 141 ||||||| 463 EDTDPRR 469

RESULT SY AC OZ SYE_METTH STANDARD; PRT; 553 MA.

57E_METH STANDARD; PRT; 553 MA.

15-UUL-1998 (REL. 36, CREATED)
15-UUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-UUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-UUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-UUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
15-UUL-1998 (REL. 36, LAST ANNOTATION UPDATE)

US-08-951-733-14.rap

0

415 EEILAKF 421 ||||||| 560 EEILAKF 566

Query Match 0.7%; Best Local Similarity 100.0%; Matches 7; Conservative Score 7; DB 1; Length 552; Pred. No. 4.47e+00; 0; Mismatches 0; Indels Indels

0

0

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Dec 21

09:28:24

U8-08-951-733-14.rap

(GLORS), OS MTISI. GLTX OS MTISI. METHANORACTERIN, THERMONITOTROPHICUM. ANCINERACTERIA, EURYARCHAROTA, METHANOBACTERIALES: METHANOBACTERIACEAE.

PEDUINCE PRON N.A.

PEDUINCE PRON N.A.

C STRAIN-DEZIA H.

A. SALTE D. R., DOUGETTE-STAMN L.A., DELOUGHERY C., LEE H.-M., DUBOIS J.,

A. SALTE D. R., DOUGETTE-STAMN L.A., DELOUGHERY C., GAURE H.,

A. ALDERGOE T. BASHERANDEH R., BIANELY D., COOK R., GILBERT K.,

A. ALDERGOE T. BASHERANDEH R., BIANELY D., COOK R., GILBERT K.,

A. ALDERGOE T. BASHERANDEH R., BIANELY D., COOK R., GILBERT K.,

A. ALDERGOE R., DANNEL R., COOK A., BUSH D., SALER H., PAYMELL D., PRUBALAR S.,

BA JUNAIT R., CARUSO A., BUSH D., SALER H., PAYMELL D., PRUBALAR S.,

BA JUNAIT R., CARUSO A., BUSH D., SALER R., PAYMELL D., PRUBALAR S.,

BA JUNAIT R., CARUSO A., BUSH D., SALER R., PAYMELL D., PRUBALAR S.,

BA JUNAIT R., CARUSO A., BUSH D., SALER R., PAYMELL D., PRUBALAR S.,

BA JUNAIT R., CARUSO A., BUSH D., SALER J., SALER

Query Match 0.7%; Best Local Similarity 100.0%; Matches 7; Conservative Score 7; DB 1; Length 553; Pred. No. 4.47e+00; 0; Mismatches 0; Indels

0 Gaps 0

136 EDTDPRR 142 ||||||| 463 EDTDPRR 469

RESULT TRACE OF TRACE DESULTA. JANCER STANDARD: PRT; 562 AA.

(9513) ACER STANDARD: PRT; 562 AA.

(9513) (REL. 35, CREATED)
T 01-807-1997 (REL. 35, LAST REFORMER PRAFE;
T 101-807-1997 (REL. 35, CREATER)
R 1180-1997 (REL. 35, CREATER)
R 1180-1997

SEQUENCE FROM N.A. STRAIN-RBF-103; MEDLINE; 94292468.

Page 58

Page 57

Dec 21 09:28:24 1998

EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES

SEQUENCE PROM N.A.
KEDILME; 90375480.
AEBI M., KIRCHNER G., CHEN J.Y., VIJJ
MARTH N.C., ABELSON J.;
J. BIOL. CHEM. 265:16216-16220(1990)

DIRTRICH P.S. MULLAND J.T. HENNESSET K.M. ALLEM E. MANDON AVILES E. DERNO A. BREWNANT. CAREFOTEN J. CHEM E. CHEMI T. J.M. CHEME C. CHEM E. CHEMI T. J.M. CHEME C. CHEM E. CHEMI T. J.M. CHEME C. MANCHEL B. MANCHEL M. KOMP. C. LASHMARI D. LEW H. LIE D. MANCHAN K. KOMPTHAN M. MORGREM R. DEFFER P. OH C. PETEL F.M. MANCHAN K. KOMPTHAN M. SOSICHER R. DEFFER P. OH C. PETEL F.M. ROBERTS D. SEEL P. SCHEMM S. SENGLEM T. SKITH V. PRILEM F. MED L. ROBERTS D. DESEMBLAMES. SENGLEM T. SKITH V. ROBERTS D. MEL E. P. CHOMM M. SENGLEM T. SKITH V. ROBERTS D. DESEMBLANDES DAVIS R.M. J. SKITH V. ROBERTS D. DESEMBLANDES DAVIS RAMES. J. SKITH V. ROBERTS DAVIS RAMES. J. SKITH V. ROBERTS D. SKITH V

ENTIFICATION, AND REQUENCE OF 19-26.

REALIZES, 4230441.

REALIZES, 423041.

REA

CHAIN MET CHAIN 546 546 TRIA NGLEDTINITANS PRANSE, HITOCHRONIAL.

POR CYTOPLASHIC/NGCLEAR PORM.

POR CYTOPLASHIC/NGCLEAR PORM.

POR CYTOPLASHIC/NGCLEAR PORM.

TRIA NGCLEDTINITANSFERASE, CI

TRIA NGCLEDTINITANSFERASE, CI

TRIA NGCLEDTINITANSFERASE, CI

ROCLEAR. CYTOPLASMIC/ CYTOPLASHIC/

546 AA; 62485 MW; 0.70 Score 7; DB 1; Length 546;

Query Match

SEQUENCE

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Gaps

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0

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RESULT 46

ID DOPO_MAT STANDARD: PRT: 620 AA.
AC 095754.
AC 095754.
DT 01-FEB-1995 (REL. 11, CREATED)
DT 01-FEB-1995 (REL. 13, LAST REQUERCE UPDATE)
DT 01-FEB-1995 (REL. 15, LAST REQUERCE UPDATE)
DE 01-FEB-1995 (REL. 15, LAST REQUERCE CE 1.14.17.1) (DO
DE NTENDATIA-SE) (DBH).
DE NTENDATIA-SE) (DBH).
OS BATTUS ROWEDSIONS (PAT).
OC EUTHARIA-ROMEDATIA.
RN 1115FCCE FROM N.A.
RN LILIBCCE FROM N.A.
RX KEDLINE: 90119125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%;
Matches 7; Conservative
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STRAIN=ISOLATE 1775;
MEDLINE, 94124015.
VERSALOVIC J., LUPSKI J.R.;
GENE 136:281-286(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VENTER J.C.:

GCIENTE 268-496-512(1995).

IL FUNCTION INVOLVED IN PROTEIN EXPORT (BY SIMILARITY).

IL SUBMUTI ONE OF SEVEN SECRETORY PROTEINS (SECA-F & SECT) THAT

COMPRISE THE PROMARYOTIC PROTEIN TRANSLOCATION APPARATUS

COMPRISE THE PROMARYOTIC PROTEIN TRANSLOCATION APPARATUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLT 44

PRIL,MARIN STANDARD: PRT: 593 AA.

O08145; 195 (REL. 31, CREATED)
01-007-195 (REL. 31, LAST SOCIENCE UPDATE)
01-007-195 (REL. 31, LAST SOCIENCE UPDATE)
01-007-195 (REL. 31, LAST ANNOTATION UPDATE)
03-007-195 (REL. 31, LAST ANNOTATION UPDATE)
04-007-195 (REL. 31, LAST ANNOTATION UPDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ROCES M. B., BENETT T. K., PANNE C.M., SMITH C.J.;

J. BLACTEROM. 156.4736.4584(1994).

- PUNCTION: INVOLVED IN THE TRANSPOSITION OF THE INSERTION SECURICE CONTENTIAL.

- PUNCTION: DECLORES TO THE IS21/15408/IS1163 FAMILY OF THE TRANSPOSITION SECURITY. BELONGS TO THE IS21/15408/IS1163 FAMILY OF TRANSPOSIALS EXCEPTLY. TRANSPOSITION; DNA-BINDING; DNA RECOMBINATION. SEQUENCE 362 AA; 68998 MM; BIEB6103 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105 LAPATPA 111
||||||||
16 LAPATPA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 09:28:24 1998
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|||||||
102 LVARVLQ 108
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SENCIPECE FROM N.A.

SENCIPECE FROM N.D.

SENCIPECE FROM N.D.

PLETSCHAMN N.D.

PLETSCH
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CLEMBRY K., SUTTON G., RITZHUGH W., FILLUS C.A., OCCAYB J.D.,
SOOTH J.D., SHIRLEY R., LIU L.T., GLODEK A., KELLEY J.M.,
FEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLON E., COTYON M.D.,
THTTEBBACK T.R., HANNA M.C., NGTYEN D.T., SAUDEK D.M., SHANDON R.C.,
THE L.D., FRITCHBAN J.L., PHENANNY J.L., GEOGRAGEN M.S. MA.
THENEN C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
TENTER J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 TRANSPORT;
EN 11
EM 453
EM 475
EM 497
EM 562
EM 562
EM 585
CB 616 AA;
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473 POTENTIAL.
495 POTENTIAL.
517 POTENTIAL.
517 POTENTIAL.
518 POTENTIAL.
519 POTENTIAL.
619 POTENTIAL.
619 POTENTIAL.
619 POTENTIAL.
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619 POTENTIAL.
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Pred. No. 4.47e+00;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 7; DB 1; Length 616;
Pred. No. 4.47e+00;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U8-08-951-733-14.rap
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RESULT 47

ID REOC_SINT3 STANDARD; PRT; 626 AA.

AC 91477;
DT 01-807-1997 (REL. 35, CREATED)

DT 01-807-1997 (REL. 35, LAST REOTRICE UPDATE)

DT 01-807-1997 (REL. 35, LAST REOTRICTON UPDATE)

DT 01-807-1997 (REL. 35, LAST REOTRICTON UPDATE)

DT 01-807-1997 (REL. 35, LAST REOTRICTON UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATITITIES AND DESCRIPE AND SECONDARY
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RE J. METROSCI. RES. 25.3 95.40(1990).

CC -1- CANALTIC ACTUTIT: 3.4-DISTRIBUTION ONDADRENALINE.

CC -1- CANALTIC ACTUTIT: 3.4-DISTRIBUTION ONDADRENALINE + ASCORBATE + 0(2)

CC -1- CANALTIC ACTUTIT: 3.4-DISTRIBUTION ONDATE: + 12)0.

CC -1- CANALTIC ACTUTIT: 3.4-DISTRIBUTION ONDATE: + 12)0.

CC -1- SUBGRIETI ROWNITERANTE.

CC -1- SUBGRIETI ROWNITERANTE.

CC -1- SUBGRIETI ROWNITERANTE.

CC -1- SUBGRIETI CHEMARY HIS CHEMARY BOUTH FORM HAY BE

CC -1- SUBGRIETI AN UNCLANDED SIGNAL SEQUENCE: - THE ADRENAL MEDULIA

CC -1- SUBGRIETI CHEMARY HIS CHEMARY BUTTO NERVAL MEDULIA

CC -1- SUBGRIETI CHEMARY HIS CHEMARY BUTTO NERVAL MEDULIA

CC -1- SUBGRIETI CHEMARY HIS CHEMARY BUTTO NERVAL MEDULIA

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CC -1- SUBGRIETI CHEMARY DE CHEMARY BUTTO NERVAL MEDULIA

CC -1- SUBGRIETI CHEMARY DE CHEMARY BUTTO NERVALINE DE CHEMARY BUTTO NERVAL MEDILIA

CC -1- SUBGRIETI CHEMARY DE CHEMARY BUTTO NERVAL MEDILIA

CC -1- SUBGRIETI CHEMARY DE CHEMARY BUTTO NERVAL MEDILIA

CC -1- SUBGRIETI CHEMARY DE CHEMARY BUTTO NERVAL MEDILIA

CC -1- CALLO NERVAL MEDILIA

CC -1- SUBGRIETI CHEMARY DE CHEMARY BUTTO NERVAL MEDILIA

CC -1- SUBGRIETI CHEMARY BUTTO NERVAL MEDILIA

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NOL MICROSOT. 01.40.355(1993).

1- FUNCTION: DNA PRIMASE IS THE POLYMEI

REPLICATION FORKS DURING CHROMOSOM.

1- COPACTON: BINDS ONE MOLE OF ENTRY FRANCHER

1- SUBDIVIT: MONOMER (BY SHILLARITY).

EMBL. L11044 J. NOT. MNOTATED.CDS.

EMBL. L11041, 18072. MNOTATED.CDS.

THE JUNIOR, 83180; 7
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PASSOJARIN STANDARD; PRT; 616 AA.

P44591:
10.1007-1395 (REL. 32, CREATED)
10.1007-1395 (REL. 33, LAST SQUIDNCE UPDATE)
10.1007-1395 (REL. 33, LAST SQUIDNCE UPDATE)
10.1007-1395 (REL. 33, LAST ANNOTATION UPDATE)
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170 VLVHLLA 176
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SEQUENCE FROM N.A.
STRAIN=RD / KW20;
HEDLINE; 95350630.
PLEISCHMANN R.D., 3
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PRESPICATION (BY CAN-KINASE)
(POTENTIAL),
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Pred. No. 4.47e+00;
0; Mismatches 0; Indels
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POTENTIAL.
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COPPER (POTENTIAL).
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Pred. No. 4.47e+00;
0; Mismatches 0; Indels
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PRAGMENTS ON BOTH TEMPLATE STRANDS
OMDSOMAL DNA SYNTHESIS.
SINC PER MOLECULE (BY SIMILARITY).
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Gaps

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CC -- SPECILLATION OF MEDICOTRANSUTTER RELEASE.

CC -- STRANGIN I IS THE SUBSTRATE OF AT LEAST FOUR DIFFERENT PROTEIN

CC KINASS, IT IS PROBABLE THAT PROSPROITATION PLAYS A ROLE IN THE

CC KINASS, IT IS PROBABLE THAT PROSPROITATION PLAYS A ROLE IN THE

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Best Local Similarity 100.0%;
Matches 7; Conservative
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005000;
01F2D-1995 (REL. 31, CREATED)
01F2D-1995 (REL. 31, LAST SEGURNCE UPDATE)
15-UT-1995 (REL. 36, LAST ANNOTATION UPDATE)
15-UT-1996 (REL. 36, LAST ANNOTATION UPDATE)
00500ENTE CANAL (FRANZENT).
01000ENTE CANAL (FRANZENT).
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1- CATALTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N PTROPHOSPHATE +
RMA(N):
1- SUBBUT: TH CYANOBACTERIA THE BNA BOLFMERASE IS COMPOSED OF POUR
SUBDULIS: ALPHA, BETA, GAMMA, AND DELTA.
EMBL: D30913: 0163355; --
EMBL: D30913: 016355; --
EMBL: D30913: 01635; --
EMBL: 
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SECURE: 9766130: KOTANI H., TANKKA A., ASAMIEU E., NAMAMURA Y.,
AMERO T., SATO E., KOTANI H., SAGUDTA H., SAGMOTO S., KIMURA T.,
MARINO T., MATUNO A., MURANI A., MARAMATI N.,
KARDO K.,
KARDO K., TARECIEI C., WADA T., WATANABE A.,
OKUMURA S., SHIMPO S., TARECIEI C., WADA T., WATANABE A.,
PANADA M., TARECIA M., TENDETA S.;
PANADA M., 1950-166(1995).
1- PUNCTION: DNA. PERFENDENT RIA POLYMERASE CATALIZES THE TRANSCRIPTION
OF DIA LIND RIA USING THE FOUR RIBONDCLEDSIDE TRIPROSPHATES AS
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558 LREETLA 564
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TRANSCRIPTION; DNA-DIRECTED RNA POLYMERASE.
SEQUENCE 626 AA; 70978 MW; C8C9ED66 CRC32;
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STRECHOCTSTIS SP. (STRAIN PCC 6003).
PROMATOTA: GRACILICUTES; OXTPHOTOBACTERIA;
CLANOBACTERIA (BLUE-GREEN ALGAE); CHROOCOCCALES.
CLANOBACTERIA (BLUE-GREEN ALGAE);
33 PPPAAPS 39
1111111
86 PPPAAPS 92
                                                                                                                                                                                                                                                                                    551
568
605
662
671
706 AA;
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113
657
657
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568
605
670
706
74518 MW;
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PHOSPHORILATION (BY CAM-KINASE II).
PHOSPHORILATION (BY CAM-KINASE II).
PHOSPHORILATION (BY CAM-KINASE II).
NISOSLINA - KARPAJAPO (IN SYNAPSIN IB
MISOSLINA - KARPAJAPO (IN SYNAPSIN IB
MISOSLINA - CACAJ:
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C (ACTIN-BINDING AND STRAPTIC-VESICLE BINDING).
D (PRO-RICH).
E.
                                                                                                                                          Score 7: DB 1: Length 706;
Pred. No. 4.47e+00;
O: Mismatches O: Indels
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RESULT ID YK AC P3 DT 01

LT 50 YKF4_YEAST STANDARD; F P35732; O1-JUN-1994 (REL. 29, CREATED)

PRT; 738 ζ

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STALLWESSES STATE

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306 SLEGALS 312
349 VAAPEEE 355
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457 VAAPEEE 463
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01-FEB-1996 (REL. 33) LAST ANNOTATION UPDATE)
REPORTETAL 84.0 KD PROTEIN IN NUPLIO-CSEM INTERGENIC REGION
TALOSAC ON TALOS.
SACCHAROFTCES CERVISIZE (BAKER'S TEAST).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 09:28:24 1998
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MEDILIE, 981005 C.B., HOGALA H., SMAGULA C.S., SUDHOF T.C.,

DEIERHOURE 31,

17.977-984(1959).

PROG.71.17.977-984(1959).

BINDS TO THE CITOSLELION, AND IS BELIEVED TO FUNCTION IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SECUENCE FROM N.A.
TISSUE-BRAIN
REDILINE, 09398255.
SUEDIDF T.C., CRERNIK A.J., KAO H.-T., TAKZI K., JOHNSTON P.A.,
ROBLICHI A., KANAER S.D., WAGNEN N.A., PERIN M.S., DE CAMILLI P.,
GREENARD P.
                                                                                                                                                                  Score 7; DB 1; Length 738; Pred. No. 4.47e+00; O; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 7: DB 1: Length 692;
Pred. No. 4.47e+00;
0; Mismatches 0; Indels
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SQ SEQUENCE 1132 AX; 126537 MM; CLESEZAF CRC32; Query March 92.3%; Score 876; D8 4; Length 1132; Best Local Similarity 99.9%; Pred. No. 0, 00e+00; Matches 926; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	00 601 LSEADYRGHEARPALLTSRLØTIFFFDGLAFTYWARTFREKARELTSRVA, 660 662 LSEADYRGHEARPALLTSRLØTIFFFDGLAFTYWARTFREKARELTSRVA, 662 07 623 LSEADYRGHEARPALLTSRLØTIFCHAMPTYLAFRAGDPPELTYWYGAADTI 7.00 663 LSEALYRGHEARREGLAGAVIGLODIHAMRTFYLAFRAGDPPELTYWYGYGATDT 7.00 664 LSEALYRGHEARREGLAGAVIGLODIHAMRTFYLAFRAGDPPELTYWYGYGATDT 7.01 665 LSEALYRGHEARREGLAGAVIGHDIHAMRTFYLAFRAGDPPELTYWYGYGATDT 7.02 666 LSEALYRGHEARREGLAGAVIGHDIHAMRTFYLAFRAGDPPELTYWYGYGATDT 7.02 660 LSEALYRGHEARREGLAGAVIGHDIHAMRTFYLAFRAGDPPELTYWYGYGATDT 7.02 661 LSEALYRGHEARREGLAGAVIGHDIHAMRTFYLAFRAGRYSTUTLAGPHAGPYAHL 8.02 662 LSEALYRGHEARREGLAGAVIGHDIHAMRTFYLAFRAGRYSTUTLAGPHAGPYAHL 8.02 663 LSEALYRGHEARREGLAGAVIGHDIHAMRTFYLAFRAGRYSTUTLAGPHAGPYAHL 8.02 664 LSEALYRGHEARREGLAGAVIGHDIHAMRTFYLAFDRAGRYSTUTLAGPHAGPYAHL 8.02 665 LSEALYRGHEARREGLAGAVIGHDIHAMRTFYLAFDRAGRYSTUTLAGPHAGPYAHL 8.02 666 LSEALYRGHEARREGLAGAVIGHDIHAMRTFYLAFDRAGRYSTUTLAGPHAGPYAHL 8.02 667 LHILLIHAMRT 111111111111111111111111111111111111	Non Dec 21 09:28:25 1998 U8-08-951-733-14.rapt	988 6 0.6 22512 1 000000 PROSIDERTRY 5.10002 970 6 0.6 25513 5 02768 PROTOCOCCOMP 578 510002 971 6 0.6 25513 5 02768 PROTOCOCCOMP 578 510002 972 6 0.6 25513 5 02768 PROTOCOCCOMP 578 510002 973 6 0.6 25513 5 02768 PROTOCOCCOMP 578 510002 974 6 0.6 25513 5 02768 PROTOCOCCOMP 578 510002 975 6 0.6 20513 1 900000 PROTOCOCCOMP 55 510002 976 6 0.6 3110 1 000000 PROTOCOCCOMP 55 510002 977 6 0.6 3110 1 000000 PROTOCOCCOMP 55 510002 977 6 0.6 3110 1 000000 PROTOCOCCOMP 55 510002 977 6 0.6 3110 1 000000 PROTOCOCCOMP 55 510002 977 6 0.6 3110 1 000000 PROTOCOCCOMP 55 510002 977 6 0.6 3110 1 000000 PROTOCOCCOMP 55 510002 977 6 0.6 3110 1 000000 PROTOCOCCOMP 55 510002 978 6 0.6 3110 1 000000 PROTOCOCCOMP 55 510002 979 6 0.6 3110 1 000000 PROTOCOCCOMP 55 510002 970 6 0.6 3110 1 000000 PROTOCOCCOMP 55 510002 970 6 0.6 3110 1 000000 PROTOCOCCOMP 55 510002 970 6 0.6 3110 1 000000 PROTOCOCCOMP 55 510002 970 6 0.6 3110 1 000000 PROTOCOCCOMP 55 510002 970 6 0.6 3110 1 000000 PROTOCOCCOMP 55 510002 970 6 0.6 3110 1 000000 PROTOCOCCOMP 55 510002 970 6 0.6 3110 1 000000 PROTOCOCCOMP 55 510002 970 6 0.6 3110 1 000000 PROTOCOCCOMP 55 510002 970 6 0.6 3110 1 000000 PROTOCOCCOMP 55 510002 970 6 0.6 3110 1 000000 PROTOCOCCOMP 55 510002 970 6 0.6 3110 1 000000 PROTOCOCCOMP 55 510002 970 6 0.6 3110 1 000000 PROTOCOCCOMP 55 510002 970 6 0.6 3110 1 00000000 PROTOCOCCOMP 55 510002 970 6 0.6 3110 1 00000000 PROTOCOCCOMP 55 510002 970 6 0.6 3110 1 000000000 PROTOCOCCOMP 55 510002 970 6 0.6 3110 1 0000000000000000000000000000000	TOP OF AN VOIGNIAN AND UP TO TOP TO TO TOP TO TO TOP TO TO TOP TO TO TOP TO TO TOP TO
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RESULT 3

ID 035432 PRELIMINARY: PET: 67 AA.
AC 035432 PRELIMINARY: PET: 67 AA.
AC 035432 PRELIMINARY: PET: 67 AA.
AC 035432 PRELIMINARY: PET: 67 AA.
DT 01-JAN-1998 (TREMBLREL. 05, LAST SHOURCE UPDATE)
DT 01-JGC-1998 (TREMBLREL. 05, LAST SHOURCE UPDATE)
DT TELOMERASE CATALUTIC SUBUNIT (FRANCHET).
OS HUS MUSCULUS (MOUSE).
OC EUTHARYOTA. METALDAI. CHORDATA: VERTESBATA: TETRAPODA: MAMMALIA:
EUTHARYOTA. METALDAI. CHORDATA: VERTESBATA: TETRAPODA: MAMMALIA:
EN SAUDENCE FROM N.A.
BASSIS N. CCLETELAND J.L.:
BA
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10 070312 PRELIMINARY; PRT; 1122 AA.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.3% Score 22; DB 11; Length 67;
Best Local Similarity 100.0% Fred. No. 2, 62e-42;
Matches 22; Conservative 0; Mismatches 0; Indels
opery Match 0.9%; Score 9; DB 4; Length 632;
Best Local Similarity 100.0%; Pred. No. 6.15e-04;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE R., CLEFFELAND J.L.;
SUBMITTED (CCT.1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
SUBMITTED (CCT.1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
BUBL: ARO39215; C2605903;
NOM_TER 67 67
SEQUENCE 67 AA; 8368 MM; E2A06F2B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COL4492 PRELIMINARY; PRT; 632 AA.

OL4492: (PERSILEEL 05, CREATE)

OL-JNN-1988 (PERSILEEL 05, LAST SECURINE UPDATE)

OL-JNN-1988 (PERSILEEL 06, LAST ANDOTATION UPDATE)

APS COMPLETE (UDAN),

DUANTOTA: HETALOD,: CHORDATA; VERTESRATA; TETRAPODA; MAMALIA;

DURINETAL; PRINATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 LAFGFALLD 16
||||||||||
119 LAFGFALLD 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

HEDLINE: 873098).

HEDLINE: 873098).

PROC. NATL. ACAD. SCI. U.S.A. 84.5354-5358(1987).

PROC. NATL. ACAD. SCI. U.S.A. 84.5354-5358(1987).

SIGNAL HATSON SERVICE POPERTIAL.

SIGNAL J. ATERNATIVE SPLICE POPERTIAL.

SIGNAL J. 24.583 LT-5 GLYCOPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 09:28:25 1998
                                                                                                                                        SEQUENCE FROM N.A.
MEDILHR. 97377002.
YOKODCHI M., SUJUKI R., MASUHARA M., KOMIYA S., INOUE YOKHOCHE A.; SUJUKI R., MASUHARA M., KOMIYA S., INOUE ZOKOCZERE 157-15(1997).
EMBL. ABOODS20; DIDZISBI: -
FRAM: PFOROUT; SHI.
FRAM: PFOROUT; SHI.
SEQUENCE 633 AA: 67727 MM; AB4DBOBD CRC33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN 24 >183 LY 5 GLYCOPROTEIN.
NOW TER 183 183
SEQUENCE 183 AA; 18601 MW; 37DE42ED CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      781 QETSPLROMVVIDOSSILMANSCLEPVFLAPHCHHAVRIRGKSTVOCOGIPQGSILGTI 800 QETSPLROMVVIDOSSILMANSCLEPVFLAPHCHHAVRIRGKSTVOCOGIPQGSILGTI 862 801 QETSPLROMVVIDOSSILMANSCLEPVFLAPHCHHAVRIRGKSTVOCOGIPQGSILGTI 862
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IRECULT:

OCIBIS.

PRELIMINARY:

PRT:

AC GOIBS.

PT 01-809-1996 (TRENDILEEL. 01 CREATED)

DT 01-809-1996 (TRENDILEEL. 01 LAST SEQUENCE UPDATE)

DT 01-809-1996 (TRENDILEEL. 01 LAST SEQUENCE UPDATE)

DE TRANSHEMENTE GLYCOPROTEIN (FRACHENT).

OC EUGAROTA, HEALOGA, CUORDATA; VERTEBRATA; TETRAPODA; HAS MUSCULTS, RODENTIA.

RN (1)

RN SEQUENCE FROM R.A.

RX MEDLINE: 89996865.

RA MEDLINE: 89996865.

RH MOL. CELL. SIGL. 8189: 4895(1989).

RR SEQUENCE TOWN G. 554192: --

PR MOLERE S. 554192: --

RA MEDLINE: 89986865.

RA MEDLINE: 89986865.

RA MEDLINE: 89996865.

RA
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RESULT 9

ID 011339 PRELIMINARY; PRT: 989 AA.

AC 011339 (TREMELREL 05, CREATED)

DT 01-JAN-1998 (TREMELREL 05, LAST SEQUENCE UPDATE)

DT 01-JAN-1998 (TREMELREL 05, LAST ANDOTATION UPDATE)

DT 01-JAN-1998 (TREMELREL 05, LAST ANDOTATION UPDATE)

ET TELOMERASE REVERSE TRANSCRIPTASE 1.
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Best Local Similarity 100.0%;
Matches 9; Conservative
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Best Local Similarity 100.0%;
Matches 9; Conservative
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Best Local Similarity 100.0%; Pred. No. 2.62e 42;
Matches 22; Connervative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 LAFGFALLD 18
|||||||||
119 LAFGFALLD 127
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013339 PRELIMINARI PRT: 988 A.
013339 PRELIMINARI PRT: 988 A.
013339 PRELIMINARI PRT: 988 A.
01-JAN-1998 (TREMBLEEL OS, CREATED)
01-JAN-1998 (TREMBLEEL OS, LAST SEQUENCE UPDATE)
01-JON-1998 (TREMBLEEL OS, LAST SEQUENCE UPDATE)
TELOMERASE REVERSE TRANSCRIPTASE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2
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MEDLIER: 9996662.
SACA T., TOWA J.S., SHEN F.W.W., PANCOAST T.C., DOTSE E.A.;
MCL. CELL. BLOL. 8:489-4895(1989).
EMDL. MINISTER MATERIATIVE SPLICING: TRANSMEMBRANE.
MON_TER
404 24
SEQUENCE 24 AA: 2717 MM; 7ALODDDA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., ALLSOPP R.C., CHIN L., MORIN G.B., ONCOCENE 0:0-0(1998).
EMBL; AFOSI911: G3005592: --
RNA-DIRECTED DAN POLYMERASE.
SEQUENCE 1122 AA; 127977 NM; 222075D6 CRC32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGUNES FROM N.A. BARBELL B.G., VOLCHAERT G.;
STRANN-972H, PAJANDREAM A., BARBELL B.G., VOLCHAERT G.;
STRANTED (NAM-1598) TO EMBL/GENBANKJOBBJ DATA BANKS.
EMBL. APOL578; C2140188;
EMBL. ALO2159; EL185180; -
BTAIL: PROPOTFS; ETC.
RNA-DIECTED DAN POLTHERASE.
SEQUENCE 988 AA; 116338 MW; 39C385A7 CRC32;
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DURARTOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: HAMMALIA:
EUTHERIA; RODENTIA.
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                               703 GIPQGSILS 711
||||||||
852 GIPQGSILS 860
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GERALHS-972H.
GERALHS-973H.
KARAMURA T.M., MORIW G.B., CHAPMAN K.B., WEINRICH S.L., ANDREWS W.H.,
LIMBURE J., HARLEY C.B., CECH T.R.;
SCIENCE 277:355-359(1957).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUTHERIA; RODENTIA.
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||||||||
719 VRAQDPPPE 727
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EUXARYOTA; FUNGI; ASCONYCOTINA; HEMIASCONYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09:28:25 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 9; DB 3; Length 988;
Pred. No. 6.15e-04;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 9; DB 11; Length 24;
Pred. No. 6.15e-04;
0; Mismatches 0; Indels
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Mon

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SEQUENCE PROM N.A.

STRAIMS-973H: ...

STRAIMS-973H: ...

MEDLINE: 97400623

MEDLINE: 97400623

MEDLINE: 97400623

MEDLINE: 97400623

MEDLINE: 97400628

MEDLINE: 974
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EUKARYOTA; FUNGI; ASCONYCOTINA; HEMIASCONYCETES.
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Overy Match 0.9%; Score 9; DB 3; Length 989; Best Local Similarity 100 Ob; Pred. No. 6.15e-04; Matches 9; Conservative 0; Mismatches 0; Indels

0

Gaps

0

8 8

SECURME FROM N.A.
ZEBEDEZ S.L. PARRITT D.S., RASCHEZ N.C.;
ZEBEDEZ S.L. PARRITT D.S., RASCHEZ N.C.;
ZEBL. PARRITS (1.1243-254(1.1911).
ZEBL. PARRITS (1.1910).
ZEBL. PERMIS (1.1910).
ZEBL. PROSER (1.1910).
Z

: PF00102; Y_phosphatase. AL; HYDROLASE. AL 1 23

SEQUENCE 1 23 POTENTIAL. 24 1291 LYMPHOCYTE COMMON ANTIGEN 1291 AA; 144559 MW; 63481A8D CRC32;

Query Match 0.9%; Score 9; Best Local Similarity 100.0%; Pred. No. DB 11; Length 1291; 6.15e-04;

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MOB MOB

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EMBL. M31151 C387402 JOINED
EMBL. M31151 C387402 JOINED
EMBL. M31154 C387402 JOINED
EMBL. M31155 C387402 JOINED
EMBL. M31156 C387402 JOINED
EMBL. M31156 C387402 JOINED
EMBL. M31156 C387402 JOINED
FAM: PFO01021 Cphosphatase.
MSMRM. PFO01021 Cphosphatase.
MSMRM. PFO11031 Table M3156 C387402 JOINED
EMBL. M3156 C354185 ...
MSMRM. PFO1001 Table M3156 C354185 ...
MSMRM. PFO1003 Table M3156 C354185 ...
MSMRM. PF
1343 1343
1343 AA; 150679 MW; 984DFAEB CRC32;
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O.9%; Score 9; DB 11; Length 1343; Best Local Similarity 100 0%; Pred. No. 6. 15e-04; Matches 9; Conservative 0; Mismatches 0; Indels 0; Caps 0

8 LAPGPALLD 16 |||||||| 119 LAPGPALLD 127

CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE) PRT; 146 AA

₽., CALVO V., VINUELA E.

SENCHMEN FROM N.A.
STRAIN-BAJYY
MEDILINE; 9019205.

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SEQUENCE FROM N.A.
STRALMSA71V;
MEDLINE, 90219204.
ALMENDRAL J.M., ALMAZAN F., BI
J. VIROL. 64:2064-2072(1990).

BLASCO R.,

SEQUENCE FROM N.A.
STRAINEATIV:
MEDINE: 91134988.
CAMACHO A., VINUELA E.;
CAMACHO TEL:251-257(1991).

EQUENCE FROM N.A. STRAIN-BA71V; LLMAZAN F., MURGUIA J.R., J., GEN. VIROL. 0:0-0(0).

RODRIGUEZ J.M.,

5

VEGA

VINDELA

8 B

SEQUENCE FROM N.A.
STRAIMS BAITY:
MEDITHE: 94.187118.
RODRIGEZ J.M., YANEZ R.J., PAI
VINUELA E.
J. VIROL. 68:2746-2751(1994).

PAH R.,

PRICAN SWINE FEVER VIRUS (ASFV). TRIDAE; DS-DNA MONENVELOPED VIRUSES; IRIDOVIRIDAE.

YUSTE L., ENRIQUEZ

SEQUENCE FROM N.A.
STRAIN-BA771:
STRAIN-BA771:
LA VEGA I., GONZALEZ A., BIASCO
VIROLOGY 201:152-156(1994).

EQUERCE FROM N.A.
TRAIN-BA'IV;
NAEZ R.J., RODRIGUEZ J.M., NOGAL M.L.,
DDRIGUEZ J.F., VINUELA E.;
INCLOST 208:249-278(1995).

RESULTA 12

ID 065310

PRELIMINARY;

AC 065210

DT 01-NOV-1996 (TRENBLEEL. 01 LA

DT 01-NOV-1996 (TRENBLEEL. 07 LA

DE PD146L.

GN PARICAN SHIRE FEVEN VIRUS

OC VIRILDE, 199-10M NONENVELOPED V

RN 121 POUR 199-10M N. A.

RC STRAIN-BAJIV;

RN 121 POUR 121-196(1994).

RN 131

R

BOCKAMP E.O., SIMON-MATEO

SEQUENCE FROM N.A.
STRAINEBAILE
MEDLINE; 93277388.
MUNCZ M., FREIJZ J.M., SALAS M.L.,
ARCH. VIROL. 130:93-107(1993).

VINUELA

SEQUENCE FROM N.A.
STRAINSANTIV;
MEDINE: 94065556.
ALCAMI A., ANGULO A., VINUELA E.;
J. GEN. VIROL. 74:2317-2324(1993)

SERDIEME FROM N.A. SERALMERATIVE, 93346971. TANEE R.J., RODRIGUEZ J.M., RODRIGUEZ J.F., SALAS M.L., VINUELA E.; J. GEN. VIROL. 74:1833-1838(1993).

SEQUENCE FROM N.A.
STRALMBATIV.
STRALMBATIV.
MEDILHE: 90357780.
BLASCO R., LOPES-COTIN C., MUNOZ M
VINUELA E.;
VINUELA E.;
112)

[12] SEQUENCE FROM N.A. STRAIN-BA71V;

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Page 29

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Page 30

0 Indels

ę. Gaps 0

9; Conservative 0 Mismatches

8 LAPGFALLD 16 |||||||| 119 LAPGFALLD 127

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Best Local Similarity 100.0%; Pred. No. 1.03e-01;
Matches 8; Conservative 0; Minnatches 0; Indels
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Best Local Similarity 100.0%;
Matches 8; Conservative
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065547 PRELIMINARY: PRT: 338 AA.
065547 PREMIMINARY: PRT: 318 AA.
065547 PREMIMINARY: PRT: 318 AA.
01.NOV-1906 (PREMIMINE: 01, CREATED)
01.NOV-1906 (PREMIMINE: 01, LAST SEQUENCE UPDATE)
01.NOV-1906 (PREMIMINE: 07, LAST ANNOTATION UPDATE)
01.NOV-1906 (PREMIMINE: 07, LAST ANNOTATION UPDATE)
01.NOV-1906 (PREMIMINE)
01.NOV-1906 (PREMIMINE)
VINIDAR: DS-DNA ENVELOPED VIRUSES: HERPESVIRIDAE: ALPHAHERPESVIRINAE.
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|||||||
142 RSYLPHTV 149
                                                                                                                                                                    083745; PRELIMINARY: PRT: 342 AA.
083745; OL-NOV-1996 (TREMCLEEL OL, CREATED)
01-NOV-1996 (TREMCLEEL OL, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMCLEEL OL, GAST ANNOTATION UPDATE)
01-NOV-1996 (TREMCLEEL OL, GASTA ANNOTATION UPDATE)
01-NOV-1996 (TREMCLEEL OL, GASTA ANNOTATION UPDATE)
MYELOPROLIFERATIVE SARCOMA VIRUS.
VIRIANE: 58-NA ENVELOPED VIRUSES: POSITIVE-STRAND; RETROVIRIDAE;
ONCOVERINAE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       270 ARRRGGSA 277
||||||||
|11|||||||
|243 ARRRGGSA 250
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STRAIN-BAILY.
MEDLINE; 94133986
RODRIGUEL J.H., YANEE R.J., F
GENE 136:103-110(1993).
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STRAIN-BA71V;
MEDLINE; 93233210.
PRADOS P.J., VINUEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STROIMNE FROM N.A.
STRAIN-COOPERS
KHADR A., TIXOO S.X., BABIUX L.A., HURK S.;
GENE 0.0-0(0).
SENGL: 014593; G114326; -.
SENGLENCE 318 AA. 35930 MH; 4F818424 CRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=BA71V;
MEDLINE; 93174976.
WANEZ R.J., VINUELA E.;
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Yanez R.J., BOURSNELL M., NOGAL M.L., YUSTE L., VINUELA E.;
NUCLEEC ACTOS RES. 21:2433-2427(1995).
SEQUENCE FROM N.A.
MEDLINE: 84216451.
STACEY A., ARBUTHNOTT C., KOLLEK R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQUENCE FROM N.A.
TRAIN-BA71V;
EDLINE; 93327788.
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ETRIAIN-BATJU;

ETRIAIN-BATJU;

ETRIAIN-BATJU;

CODRIGUEZ J.M. YANEZ R.J., ALMAZAN F.,

VEROL. 67:5312-5320(1993).
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INON-MATEO C., ANDRES G., VINUELA E.;
MBO J. 12:2977-2987(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQUENCE FROM N.A.
TRAIN-BA71V;
EDLINE; 90223993.
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TEALTH-SATURE; 92360660 ... LOPEZ-OTIN C.,
LEANI A., ANGULO A., LOPEZ-OTIN C.,
ARRASCOSA A.L., VINDELA E.;
VIROL. 66:3860-3868(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DPEZ-OTIN C., FREIJE J.M.,
IROLOGY 175:477-484(1990).
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ANEZ R.J., RODRIGUEZ J.M.,
ENE 134:161-174(1993).
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DOS F.J., VINUELA E., ALCAMI A.;

VIROL. 67:2475-2485(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93; G1143226; -.
338 AA; 35930 NW; 4F818424 CRC32;
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Pred. No. 1.03e-01;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RODRIGUEZ J.F., VINUELA E., SALAS M.L.;
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            COGGINS L., OSTERTAG W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MUNOS M., PREIJE J.H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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O 01324

PRELIMINARY; PRT: 508 AA.

AC 01324

DT 01-301-1997 (TREBLEZI. 04, CREATED)

DT 01-301-1997 (TREBLEZI. 04, LAST SEQUENCE UPDATE)

DT 01-301-1997 (TREBLEZI. 04, LAST SEQUENCE UPDATE)

DT 01-301-1998 (TREBLEZI. 04, LAST ANDTATION UPDATE)

DE CYTOCHRONE P450 SCC [CC 1.14.14.1).

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RE 115-10-1908

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            RESULT 16
ID 015740
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                                                                                                                                                                                                                                                                                                                                   Query Match 0.8%;
Best Local Similarity 100.0%;
Matches 8; Conservative
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Best Local Similarity 100.0%;
Matches 8; Conservative
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STRAIN-BA71V;
NEDLINE; 92007485,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (23)
SECUTANCE PROM N.A.
SECUTANCE PROMISSION
SECULINE: 92363807
CARCIA-BEATO R., FREIJE J.M., L
SALAS M.L.,
CARCIA-BEATO R., 978218 J.M., L
TANDAS M.L.,
CARCIA-BEATO R., 978218 J.M., L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIANE 97208876

MEDIANE 97208876

MEDIANE 97208876

CERE 185:317-322(1997)

1- SHILARITE BELOGG TO THE CITOCHROME P450 FAMILY.

EMBL. P49001 521096771

EMBL. P49001 521096771

EMBL. P49001 521096771

EMBL. P49001 52109671

EMBL. P5900871

EMBL. P590087
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||||||||
372 LRPSLTGA 379
                                                                                                                                                                           128 PYGVLLKT 135
|||||||
426 PYGVLLKT 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. VIROL. 50:725-732(1984).
EMDL. KO1683: G332293: -
EMDL. KO1683: G332293: -
PROSTITE: P8001069: PACTRIN, IINASE_ST: 1.
PSPAH: PP000659: PALTAMA.
COAT PROFERIM: EMPTLADPE PROFERIM
SEQUENCE 342 AA: 37871 MM; 90P93921 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEDIENCE FROM N.A.
STRAINENATIVE
MEDILHE: 97016328.
GONRALER A., TRANTERA A., ALMENDRAL J.M., VINUELA E.;
FROLIZIC ACIES RES. 14:6835-6844(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SENDIENCE FROM N.A.
STRALINBAJIVI,
KINEE R.J.
KINEE R.J.
SCHRITTED (DEC-1994) TO EMBL/GENBANK/DDBJ DATA BANKS
EMBL; U18486; G780518; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VIROLOGY 193:531-536(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEROIENCE FROM N.A.
STRAINBAÎLY.
FRELTE: 94091056.
FRELTE J.M. LAAN S. VINDELA E., LOPEE-OTIN C.:
VIRUS RES. JO:63-72(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEDÚENCE PROM N.A.
STRAINHBATIV:
MEDLINE: 95159428.
MEDLINE: 95159428.
SIMON-MATEO C., FREIJE J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEGLEMEZ PROM N.A.
STRAINHANIY.
DENALIE: 93174941.
DENALIE: TANES R.J., REVILLA Y., VINUELA E., SALAS M.L.;
VIROLOGI 133:313-338(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EDDENCE FROM N.A.

TEXALMENATU:

EDILINE, 95016035.

LORIGOEZ F., ALCARAS C., EIRAS A., YANEE R.J., RODRIGUEZ J.M.,

LONSO C., RODRIGUEZ J.F., ESCRIBANO J.M.;

VIROL. 68:7244-7252(1994).
      PRELIMINARY;
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Pred. No. 1.03e-01;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                         Score 8; DB 13; Length 508;
Pred. No. 1.03e-01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VINUELA E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANDRES G.,
            PRT;
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            680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-951-733-14.rapt
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ID 024144 PRELIMINARY: PRT: 869 AA.
AC 024144 PRELIMINARY: PRT: 869 AA.
AC 024144 PRT: 01 CREATED)
DT 01-NOV-1996 (TREMELREL. 01 LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMELREL. 05, LAST ANNOTATION UPDATE)
DE INTURNED PROTEIN.
GN IN.
GN
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                                                                                                                                                                                                                                                                                        Query Match 0.7%;
Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%; Pred No. 1.03e-01;
Matches 8; Conservative 0; Mismatches 0; Indels
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|||||||
364 RPSFLLS 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    015740;
01-JAN-1998 (TREMGLERI. 05, CREATED)
01-JAN-1998 (TREMGLERI. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMGLERI. 05, LAST ANNOTATION UPDATE)
PKSA (PAGHENT).
PKSA (PAGHENT).
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STEALINGA-2.
STEALINGA-2.
MINISTRAN 96059477.
MADIZIDE J. GOSTIER M.C., VAYSSIE L., HOUARI A., SPERLING L.;
MADIZIDEL L. GOSTIER M.C., VAYSSIE L., HOUARI A., SPERLING L.;
MADIZIDEL CITYLO GOSTIATO; -.
MARIXI PROTZIE GOSTIATO; -.
MARIXI PROTZIE GOSTIATO; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DICTYGOSTELIUM DISCOIDEUM (SLIME MOLD)
EURARYCTA, PROTUZOA, SARCOMASTIGOPHORA; SARCODINA; RHIZOPODA;
EUNTETOZOA; DICTYGOTELIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               430 SRSLPLPK 437
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||||||||
559 REEILAKF 566
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                                                                                                                                                                                                                                                                                               Score 7; DB 10; Length 37;
Pred. No. 1.01e+01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 7; DB 5; Length 23; Pred. No. 1.01e+01; 0; Mismatches 0; Indels
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Bda9
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                                                                                                                                                      RESULT 22

RESULT 22

RESULT 23

RESULT 24

AC G3380

DT 01-807-1996 (TREMBLEEL 01, CREATED)

DT 01-807-1996 (TREMBLEEL 01, LAST SECURACE UPDATE)

DT 01-807-1996 (TREMBLEEL 01, LAST SECURACE UPDATE)

DE HEPA (FRAMENT)

DE HEPA (FRAMENT)

OF PLASHID PECHANOZ

OF PLASHID PECHANOZ

OC FREEPCOCCCICCELE.

RN [1]

RP SECURNCE FROM N. A.

EC STRAIN-CCSA;

RA CORRELA F.F., DIRIENDO J.M., MCRAY T.L., ROSAN B.;

RH LIPECT THANN 66:2114-2111(1996).

DR EMBL: G4642; G18491; -

TH PLASHID

FOR DAMECE 109 AA: 11728 MF; DDDP9548 CRC32:
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ID 027174;
PRELIMINARY: PRT: 23 AA.
AC 027174;
DT 01-NOV-1996 (TREMBLEEL. 01, CREATED)
DT 01-NOV-1996 (TREMBLEEL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLEEL. 01, LAST SEQUENCE UPDATE)
DT TRICHOCTO'S MATRIX PROFIELN T2 (FRAGMENT).
DE TRICHOCTO'S MATRIX PROFIELN T2 (FRAGMENT).
RN 111 MATRIX PROFIELN T3 (FRAGMENT).
RN 2500ENCE FROM N.A.
RC STRALNED-1-2;
RN MEDICULNE: 95110139.
RN MEDICULNE: 95110139.
RN MEDICULNE: 95110139.
RN 1210 MATRIX T6: 329-335(1894).
RN 1210 MATRIX T6: 329-335(1894).
RN 1210 MATRIX T6: 329-335(1894).
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AC 060300; PREMIMEL. 07, C:
DT 01-NG-1998 (TREMBLEEL 07, L:
DE RIAMOSS) PROTEIN (PRACHENT).
COM DETAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dec 21 09:28:25 1998
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Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.8%;
Best Local Similarity 100.0%;
Matches 8; Conservative
Query Match 0.7%;
Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 LVAPSCA 58
|||||||
183 LVAPSCA 189
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|||||||
15 ALAPATPA 22
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052175-1998 (TREMBLEL 06, CERATE)
01-VUN-1998 (TREMBLEL 06, LAST SEQUENCE UPDATE)
01-VUN-1998 (TREMBLEL 07, LAST ANNOTATION UPDATE)
PLASHID PRETA, COMPLETE PLASHID SEQUENCE.
PLASHID PRETA, COMPLETE PLASHID SEQUENCE.
PLASHID PRETA,

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TISSUE-BRAIN.
MACABE T., ISHIKAWA K., HIYAJIWA N., TAKAKA A.,
OARRA O.;
DARA KES.
S.:31-39(1998).
DAR KES.
SERGI, ABOILLIS, D1026(09;
MON_TER
1004_TER
1095_TAA; 118835_MF; 43474254_CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLASMID.
SEQUENCE 87 AA; 9613 MW;
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STRALIMON-22: 1919139
MEDILME: 951313139
MADEZOD L. GAUTIER M.C., LE CAER J.P., DE LOUBRESSE N., SPERLING L.:
BIOCHIMIE 16:1252-135(1994).
                                                                                                                                  NON_TER 1 1
SEQUENCE 109 AA; 11728 MW; DODF954B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPÓUENCE FROM N.A.
SANRES D.E., KEASLER S.P., LAMPEL K.A.;
SUBLITITED (SEPE-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
BUBL: APO25795; G2689636; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                251 SRSLPLPK 258
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UKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
UTHERLA; PRIMATES.
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UKARYOTA; PROTOZOA; CILIOPHORA; CILIATA; HOLOTRICHA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
Score 7; DB 2; Length 109;
Pred. No. 1.01e+01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 8; DB 4; Length 1095;
Pred. No. 1.03e-01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 7; DB 2; Length 87;
Pred. No. 1.01e+01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3DE25EOA CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-951-733-14.rspt
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Page 40

Ş RESULT

21

0

Gaps 0 Gaps

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Mon Dec 21 09:28:25 1998
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63 GASVLGL 69 ||||||| 699 GASVLGL 705

US-08-951-733-14.rept

Page 41

Mon Dec 21 09:28:25 1998

Query Match 0.7%; Score 7; DB 2; Length 113; Best Local Similarity 100.0%; Pred. No. 1.01e+01; Matches 7; Conservative 0; Mimmatches 0; Indels

Indels

0

Caps

0

NON_TER 1 1 1 NOW_TER 113 113 SEQUENCE 113 AA; 11864 MW; 08A79AA1 CRC32;

US-08-951-733-14.rspt

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Page 42
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RESULT 24

IR CONTINUE TO THE 
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ID 004233

PRELIMINARY: PRT: 111 AA.

AC 004293

DT 01-NOV-1996 (TREMBLEEL. 01. CREATED)

DT 01-NOV-1996 (TREMBLEEL. 01. LAST SEQUENCE UPDATE)

DT 01-NOV-1996 (TREMBLEEL. 01. LAST SEQUENCE UPDATE)

DT 01-PED-1997 (TREMBLEEL. 02. LAST ANNOTATION UPDATE)

DE HYPOTHETICAL 12.3 AD PROTEIN.

GR 0RF 2.

GR 0RF 2.

GR 0RF 2.

GR 0RF 2.

GR 131

RF 25CUENCE FROM N.A.

RG STALEPOLILINA A.I., SEREGINA S.A., TIRMONINOVA L.P., RATURG STALEPOLICINA S.A., TIRMONINOVA L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mon
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                                                                                                                                                                                       Query Match 0.7%; Score 7; DB 3; Length 111;
Best Local Similarity 100 O%; Pred. No. 1.01e+0);
Matches 7; Conservative 0; Minmatches 0; Indels
Query Match 0.7%; Score 7; DB 2; Length 128; Beat Local Similarity 100.0%; Pred. No. 1.01e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LT 27
OSSON PRELIMINARY; PRT; AGAINGTON OSSON:
OSSON:
OSSON:
O1-NOV-1996 (TREMELEEL O1 CREATE)
O1-NOV-1996 (TREMELEEL O1 LAST SEQUENCE UPDATE)
O1-NOV-1996 (TREMELEEL O1 LAST ANNOTATION UPDATE)
HIPOTHETICAL 14.4 ND PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIF-A:
STRAIF-A:
STRAIF-A:
GRASSIY N. XIANG E., ARIYOSHI K., AABY P., JENSEN B., DIAS F.,
WHITTLE R., BREUER J:
SUBNITTED (NAY-1398) TO EMBL/GENBANK/DDBJ DATA BANKS.
BMBL: AJ008512: E1297364;
NOM.TER 125 125
NOM.TER 125 A): 13505 NH; PC04002C CRC32:
SEQUENCE 125 AA; 13505 NH; PC04002C CRC32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 PSTSRPP 13
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| 330 PSTSRPP 336
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640 TSRLRFI 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SENGUENCE FROM N.A.
STRAIN-DLI,
STRAIN-DLI,
STRAIN-DLI,
STRAIN-DLI,
STRAIN-DLI,
SEBGINA N.A., TIKHOMIROVA L.P., KRYUKOV V.M.;
SUBMITTED (API-1991) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL. X58651 G27661 .
STROIN-TICLA PROTEIN
SENGUENCE 111 AA; 12231 MM; 39D4893A CRC12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAINSA,
XIANG E., ARIYOSHI K., WILKINS A., DIAS F., WHITTLE H., BREVER J.;
XIANG RES. HUM. RETROVIRUSES 13:501-505(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VIRIDAE; SS-RNA ENVELOPED VIRUSES;
LENTIVIRINAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 09:28:25 1998
                                                                                                                                                                                         SENDIENCE FROM N.A.
STRAIN-POCESON.
STRAIN-POCESON.
SENDIEN 96127529.
SENDIEN 96127529.
SENDIEN 96127529.
SENDIEN 96127529.
SENDIEN 961005; GLOSGO777.
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YNDERCYTSTIS SP.
RROCKOCCLLES.
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IN CORREST PRELIMINARY PRT: 135 AA.

AC 08023) PRELIMINARY PRT: 135 AA.

AC 08023) PRELIMINARY PRT: 135 AA.

AC 08023) PRELIMINARY PRT: 135 AA.

DE 1907-1996 (PREMILEREL 01, CAST RESOURCES UPDATE)

DE 17-DEL LEDREMIN-LINEHONA VIRUS TIPE II (CLORE NO-5) TAX-2 (PRACHEMY).

DE 17-DEL LEDREMIN-LINEHONA VIRUS TIPE II (CLORE NO-5) TAX-2 (PRACHEMY).

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DE 17-DEL LEDREMIN-LINEHONA VIRUS TIPE II (CLORE NO-5) TAX-2 
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AC 050099: PRELIMINARY
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Best Local Similarity 100.0%; Pred. No. 1.01e+01;
Matches 7; Conservative 0; Mismatches 0; Indels
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COTISTIL PRELIMINATY PRT: 125 AA.

COTISTIC PROBLEMENT. O7, CREATED;

TOLANG 1998 (TREMPLEMEL O7, CARATED)

TOLANG 1998 (TREMPLEMEL O7, LAST ANNOTATION UP OAC PROTEIN (FRANKENT).

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152 ALRGSGA 158
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251 SRSLPLP 257
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811 AVVIEQS 817
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243 ARRRGGS 249
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MEDILIES, 923616.
MIRILIE D., CEANEY R.
J. MED. VIROL. 36:135-141(1992).
DEBL: #851985: 0229555: -.
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SECOURCE 135 AA; 14124 MW; 1885402E CRC32:
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ROBISON K.;
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PROKARTOTA; FIRMICUTES; ACTINOMYCETALES; MYCOBACTERIACEAE.
                             SEQUENCE PROM N.A.
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Pred. No. 1.01e+01;
0; Mismatches 0; Indels
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9

Page 44

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Man Dec 21 09:28:25 1998
FRANCHINI G., PELBER B.K.,
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Query Match 0,7%, Score 7; DB 14; Length 138; Best Local Similarity 100:0%; Pred. Mo. 1. 101eto; Matches 7; Conservative 0; Mismatches 0; Indels MEDINE: 95297146.
CIMMALE V. D'AGSTINO D.M., ZOTTI L., FRANCHI
CHIEDO-BLANCHI L.;
CHIEDO-BLANCHI L.;
VIROLOGY 209:445-456(1995),
EMBL. L14165 (780299; ...
SEBUL L14165 (780299; ...
SEBUCHENCE 138 AA; 14316 MM; EA0983AO CRC32; 75 SRSLPLP 81 ||||||| 251 SRSLPLP 257 9 0

RESULT ACCOUNTS OF THE PROPERTY OF THE PROPERT 107 10 04881 PRELIMINARY; PRT: 146 AA.
048881 O1-1007-1396 (TREMELREL. 01, CREATED)
01-1007-1396 (TREMELREL. 01, LAST ESQUENCE UPDATE)
01-1007-1396 (TREMELREL. 01, LAST ESQUENCE UPDATE)
101-1007-1396 (TREMELREL. 07, LAST ANOTATION UPDATE)
10A1 FROTEIN (FRACIENT).
10A1 FROTEIN (FRACIENT).
10A257ELLA ARGOZZES:
10A257ELLA GRACILICUTES; SCOTOBACTERIA: FACULTATIVELY ANAEROBIC PROMATORACCAE.

SUCAINO N.; SUTL-1995) TO ENGL/GENHANK/DDBJ DATA ENGL; DASSA4, G940401; -. ENGL/GENHANK/DDBJ DATA NON.TER 146 146 18 18712 NN; 53345260 CRC32; TRAIN-W70;

Ouery Match 0,7%; Score 7; DB 2; Length 146; Best Local Similarity 100.0%; Pred. Mo. 1.01e+01; Matches 7; Conservative 0; Mismatches 0; Indels 58 LRPSLTG 64 ||||||| 372 LRPSLTG 378 ö 0

8 B

PDT 00 082405, PRELIMINARY; PRT; 149 AA.
082405, 082406, 0824

Mon Dec 21 09:28:25 1998 US-08-951-733-14

Ouery Match

Best Local Similarity 100.0%;
Matches 7; Conservative 86 SRSLPLP 92 |||||||| 251 SRSLPLP 257 Score 7; DB 14; Length 149; Pred. No. 1.01e+01; 0; Mismatches 0; Indels

RESULT 33

ID 09335;

OR 09335; PARTIAL CDS, CLONE

HUMAN T-CELL LYMPHOTROPIC VIRUS TYPE II. VIRILDE: SS-RNA NORMYRELOPED VIRUSES; POSITIVE STRAND RNA VIRUSES; RETHOVIRIDAE, PORCOVIRINAE; TYPE C ONCOVIRUS GROUP; NAMMALIAN TYPE C ONCOVIRUSES.

STRAINS-SP1 PX;

KEDLINE; 9619054.

KEDLINE; 9619054.

CLIVERA M. P., LARREIRO P., ISHAK M., ACEVEDO V., BAMMERSHIAK M.,

ZHU S. W., KURO T., BALL W. W.;

J., VIROL. 70:1481:149213996).

ESEL, 0713873; G4463041.

Query Match 0.7%; Best Local Similarity 100.0%; Matches 7; Conservative Score 7: DB 14: Length 149; Pred. No. 1.01e+01; 0; Mismatches 0; Indels 0 Caps

0

86 SRSLPLP 92 ||||||| 251 SRSLPLP 257

RESULT
AC OR
DT 01
DT 01
DT 01
DT 01
DT 01 107 34 ORZESS.

082391 PRELIMINARY, PRT: 149 AA.

082391 PREJAMARY, PRT: 149 AA.

082391 PRT: 149 AA.

082391 PRT: 149 AA.

082391 PRT: 149 AA.

01.100-1396 (TREMELREL. 01, CREATED)

10.100-1396 (TREMELREL. 05, LAST MATOTATION UPDATE)

17-CELL LIMPHOTROPIC VIRUS TIPE 2 REX AND TAX GENES,

572 (TRANSMERT) PARTIAL CDS,

Page

Dec 21 09:28:25 1998

INDAN T-CELL LYMPROPROPIC VIRUS TYPE II VIRLDAE: SS-RNA NOMENVELOPED VIRUSES; POSITIVE STRAND RNA VIRUSES; RETROVIRIDAE: ONCOVIRINAE: TYPE C ONCOVIRUS GROUP; MANGALIAN TYPE C ONCOVIRUSES.

STRAIN-SP2 PROM N.A.
STRAIN-SP2 PX.
KEDLINE: 96190544.
KEDLINE: 96190540.
KEDLINE: 96190540.
KEDLINE: N. CAUTERN P. HONKEN C., OLIVIERA N.D., OLIVIERA O.D., ISHAK R.,
KEDLINE: OLIVIERA M.F., LAUTERNO P., ISHAK M., ACEVEDO V., HAMMERSHIAK H.,
KED S. W., KEND C., PALLA W.F. SHAK M., ACEVEDO V., HAMMERSHIAK H.,
KEND S. W., KEND C., 1645038.
KENL J. U28073. 19165038.

SEQUENCE 149 AA; 15779 MW; 5E356C3B CRC32;

Query Match 0.7%; Best Local Similarity 100.0%; Matches 7; Conservative Score 7; DB 14; Length 149; Pred. No. 1.01e+01; 0; Mismatches 0; Indels Gaps

86 SRSLPLP 92 ||||||| 251 SRSLPLP 257

CDS,

SECURNCE FROM N A.
MEDILINE: 9619054.
MEDILINE: 961

Query Match 0.7%; Score 7; DB 14; Length 149; Dec 21 09:28:25 1998

Page 45

PAR PX (FRAGMENT). REX.

Page 46

HUMAN T-CELL LYMPHOTROPIC VIRUS TYPE II.
VIRIDAE: SS-RMA MONENVELOPED VIRUSES: POSITIVE STRAND
RETROVIRIDAE: ONCOVIRURE: TYPE C ONCOVIRUS GROUP;
MANGALIAN TYPE C ONCOVIRUSES. RXA

SECURACE NOVA N.
MEDILHE: 96190544.
MEDILHE: 96190544.
OLIVIERA N.B. NOVA P. NONERS C., OLIVIERA N.D., OLIVIERA O.D.,
EIRAMU N. NOVA P. LAUREISO P., ISHAK M., ACEYEDO V., HAMCERSHLAK
RUS N. KURO T., NALL W.W.;
RUS N. KURO T., NALL W.W.;
RUS N. KURO T., OLIVIERA N.D.,
RUS N. KURO

EMBL; 032880; G1463058; -.
NON_TER 1 1
SEQUENCE 149 AA; 15672 MW; BA56CDCB CRC32;

Query Match 0.7%; Best Local Similarity 100.0%; Matches 7; Conservative Score 7; DB 14; Length 149; Pred. No. 1.01e+01; 0; Mismatches 0; Indels 0; Caps

86 SRSLPLP 92 |||||||| 251 SRSLPLP 257

RESULT 32

ID 083397

PRELIMINARY; PRT; 149 AA.

AC 083397;
DT 01-NOV-1996 (TRENDELEEL. 01. CREATED)
DT 01-NOV-1996 (TRENDELEEL. 01. LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TRENDELEEL. 01. LAST SEQUENCE UPDATE)
DE 77-CELL LYREPOTROPIC VIRUS TYPE II.

OR WINARY-1998 (TRENDELEEL. 06. LAST AND TAX GENES, PAR.

OR TREN.

OR TREN.
OR TREN.
OR TREN.
OR TREN.
OR RETAINARY SS-RNA NOMENVELOPED VIRUSSES; POSITIVE STRAND R.
OR RETAINARY-1996 (TRENDELEEL. 02. LAST AND TAX GENES, PAR.

OR RETAINARY-1996 (TRENDELEEL. 03. LAST AND TAX GENES, PAR.

RE 111
OR TREN.
OR RETAINARY-1996 (TRENDELEEL. 04. LAST AND TAX GENES, PAR.

RE 121
OR TRENDELEE FROM N. A.

RE 2501ENCE FROM N. A.

RE 2501ENCE FROM N. A.

RE 2501ENCE FROM P. HONKEN C., OLIVIERA M. D., OLIVIERA
A.

RE 2501ENCE TRENDELEE P., 1518A M., ACTUEDO V., HAMSEN
RE 2501ENCE 149 AA; 15748 MS; 3032851F CRC32; PARTIAL CDS, CLONE

REX. HUMAN T-CELL LYMPHOTROPIC VIRUS TYPE II. VIRIDAE, 88-RMA NONENVELOPED VIRUSES; POSITIVE STRAND RMA VIRUSES; RETROVIRIDAE, ONCOVIRIMAE; TYPE C ONCOVIRUS GROUP; MAMMALIAN TYPE C ONCOVIRUSES.

SEQUENCE FROM N.A.
STRAIN-MANNE PROM N.A.
STRAIN-MANNE STRAIN-MANNE P. S. SINAK R., OLIVIERA M.D., OLIVIERA O.D., ISHAK R.,
DLIVIERA M.P., LAUREIRO P., ISHAK H., ACEVEDO V., HAMMERSHLAK N.,
END S.W., KUBO T., THALL W.W.,
J. VIROL. 70.1406-1402(1996).
ENDL. 102874; G1465044; -.

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Mon Dec 21 09:28:25 1998
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US-08-951-733-14.rapt

Best Local Similarity 100.0%; Pred. No. 1.01e+01; Matches 7; Conservative 0; Mismatches 0; 86 SRSLPLP 92 ||||||| 251 SRSLPLP 257 Caps

B

RESULT 18

DRESULT 18

DRESULT 195

DRESULT 196

DRESULT 197

DRESULT

SEÑCIENCE FROM N.A.
STRAIN-ENANGO I(MAI) PX:
STRAIN-ENANGO I(MAI) PX:
EIRAKU N. NOVAO P., HONKEN C., OLIVIERA H.D., OLIVIERA O.D., ISHAK R.,
EIRAKU N. NOVAO P., HONKEN C., OLIVIERA H.D., OLIVIERA N.R.,
EIU SK., KURD T., BALL M.;
EN SK., KURD C., BALL M.;
ENDEL, TOLIKEL-1492(1996).
MML, UD2875; 01460/19.

NON_TER 1 1 SEQUENCE 149 AA; 15779 MW; SE356C3B CRC32;

8 Onery Match 0.7%; Score 7; DB 14; Length 149; Best Loss Similarity 100:04; Pred. No. 1:01e+01; Matches 7; Conservative 0; Mismatches 0; Indels <u>.</u> Caps 0

Ş 86 SRSLPLP 92 ||||||| | 151 SRSLPLP 257

RESULT 17
ID 039680 PRELIMINAN: PRT; 153 AA.
C 039680 C TREMELREL. 01 CREATED
DT 01.NOV-1396 (TREMELREL. 01 LAST SECURING UPDATE)
DT 01.NOV-1396 (TREMELREL. 07 LAST SECURING UPDATE)
DT 01.NOV-1396 (TREMELREL. 07 LAST ANNOTATION UPDATE)
DT 01.NOV-1396 (TREMELREL. 07 LAST ANNOTATION UPDATE)
ON DATE OF CONNTE (FRANCO).
S DATES CHARTOTA: PLANTA: EMBRIOPHYTA: ANGIOSPENDAE: DICOTILEDONEAE: APIALES:

Dec 21 09:28:25 1998

SERREGEROSEPE SEQUENCE FROM N.A.
TISSIDEMENTS CORD:
TUSSIDEMENTS CORD:
BRUNS D. EXCRES S. YANG C., OSSIG R., JEROMIN A.,
J. MEJEROSCI 17:1899-1910(1997).
EMBL, UBS005, 10323250;
EMBL, UBS005, 10323250;
SEQUENCE 169 AA: 17817 MM; P4C05E4B CRC32; 00.188; TREMBLEEL 04, CREATED)
01.-701.-1997 (TREMBLEEL 04, LAST SEQUENCE OPDATE)
01.-701.-1997 (TREMBLEEL 05, LAST SEQUENCE OPDATE)
01.-701.-1998 (TREMBLEEL 05, LAST MANORATION OPDATE)
STRAPOMENTY BORDLOG.
BIRDO MEDICIALLIS (MEDICIAL LEECE).
BIRDO MEDICIALLIS (MEDICIAL LEECE).
11. JAHN

Overy Match 0.7%; Score 7; DB 5; Length 169; Best Local Similarity 100.0%; Pred. No. 1.01+ch1; Matches 7; Conservative 0; Mismatches 0; Indels 0 Caps

ş B 14 GLPAPGA 20 |||||||| |237 GLPAPGA 243

PRECIOT 40

ID 073454

AC 073454

DT 01-MG-1998 (TREDBLEEL, 07, CREATED)

DT 01-MG-1998 (TREDBLEEL, 07, LAST SEQUENCE UPDATE)

DT 01-MG-1998 (TREDBLEEL, 07, LAST SEQUENCE UPDATE)

DT 01-MG-1998 (TREDBLEEL, 07, LAST ANNOTATION UPDATE)

DE REX PROTEIL LYMPHOTROPIC VIRUS TYPE 2B.

OC VIGUESS; RETROID VIRUSES; RETROVIBINAE, BLV-HTLV RETROV

OC ETHAN T-CELL LYMPHOTROPIC VIRUS TYPE 2.

RH (11)

RH SEQUENCE FROM N.A.

PROTEIL SEASONTE E., GESSAIN A., MONFLAISIR N.;

RH LIJOMENCE FROM N.A.

RH SEQUENCE FROM N.A.

RE SEQUENCE FROM N.A.

RE SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

RE SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TROM N.A.

SEQUEN HUMAN T-CELL LYMPHOTROPIC VIRUS TYPE 2B. Viruses, retrolid Viruses, retroviridas, blv-htlv retroviruses, Kuman T-Cell Lymphotropic virus tipe 2. DÉDURCE FROM N.A. HETOURNUE F. D'ANTIOL L., DAZZA M.C., PETEZES M., BEDJABAGA 1007 P., DELAPOTE E., GESSAIN A., MONPLAISIR N.; CEM. VIROL. 79:269-277(1998).

Query Match 0.7%; Score 7; DB 14; Length 170; Best Local Similarity 100.0%; Pred. No. 1.01e+01; Matches 7; Conservative 0; Mismatches 0; Indels ESOURNEE FROM N.A.
LETORINEER F. (1971) TO EMPL/GENBANK/DDBJ DATA BANKS
SUBMITTED ((NY.1397) TO EMPL/GENBANK/DDBJ DATA BANKS
SEGUENCE 170 AA: 18402 MM; BCE45442 CRC32;

US-08-951-733-14.rapt

107 SRSLPLP 113 ||||||| 251 SRSLPLP 257

Page 51

Mon

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1998

US-08-951-733-14.rept

ID 00819 PRELIMINARY;

AC 00819;
AC 00819;
AC 00819;
D7 01-NOV-1996 (TREMELEEL. 0
D7 01-NOV-1996 (TREMELEEL. 0
D7 01-PE-1970 (TREMELEEL. 0
D7 01-PE-1970 (TREMELEEL. 0
D8 REX. HOUTEN, SERVAN ENVELOPED,
CO WINTON, SERVAN ENVELOPED,
CO WINTON, SERVAN ENVELOPED,
CO WINTON, SERVAN ENVELOPED,
CO WINTON, SERVAN ENVELOPED,
RE 1200 SERVAN A. REVELOPED,
RE 1201 SERVAN A. REVELOR FROM N. A.
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REVELOR FROM N. A.
REVELOR FROM N. A.
REVELOR PRELIMINARY; 222 CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE) PRT;

HUMAN T-CELL LEUKEMIA VIRUS TYPE II (ISOLATES G12 AND NRA) (HTLV-II). VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;

BEOUTENCE FROM N.A. HEDLINE: 9333207. PARDI D., SMITEER W.M., HADLOCK K.G., KAPLAN J.E., LAL R.B., POLES T. M. 57:4659-4664(1993). J. VIROL. 67:4659-4664(1993).

SEQUENCE FROM N.A.
HEDLINE: 930444

HEDLINE: 930444

NOTEN N. MARINGE G., CAMETTI A., MARINGCI G., CHEN I.S.Y.,
NOTEN M., MAN T., LECKIE G., LAMETTI A., MARINGCI G., CHEN I.S.Y.,
NOTEN M., MAN T., LECKIE G., LAMETTI A., MARINGCI G., CHEN I.S.Y.,
NOTENBLAT J.D., T. SEQUENCE J. SEQUE

Query Match 0.7%; Best Local Similarity 100.0%; Matches 7; Conservative Score 7; DB 14; Length 170; Pred. No. 1.01e+01; 0; Mismatches 0; Indels 0; e g

0

107 SRSLPLP 113 |||||||| |251 SRSLPLP 257

RESULT 42

ID Q055(01: Q055(01

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Page 49

US-08-951-733-14.rspt

Page 50

OMBELLIFERAE.

SENCIENCE FROM N.A.
SENAIN-DANCES HALF-LONG: TISSUE-SONATIC EMERYOS AT THE GLOBULAR STAGE;
SUB-HITED (AM-1996) TO EMEL/GENBANK/DDBJ DATA BANKS.
EMBL: Q4709; 017965; EMBL: Q4709; 01796; 01

Query Match 0.7%; Best Local Similarity 100.0%; Matches 7; Conservative SEQUENCE 153 AA; 18394 MW; A7D65CA5 CRC32; Score 7: DB 10: Length 153; Pred. No. 1.01e+01; 0; Mismatches 0: Indels

0 Caps

0

23 LPRLPQR 29 ||||||| 401 LPRLPQR 407

RESULT 38

DO 07979 PRELIMINAT: PRT: 167 AA.
AD 07979 PRELIMINAT: DI CREATED

DY 01-NOV-1996 (TRENDILEEL. 01, CART REQUENCE UPDATE)

DY 01-NOV-1996 (TRENDILEEL. 01, LAST REQUENCE UPDATE)

DY 01-NOV-1996 (TRENDILEEL. 01, LAST REQUENCE UPDATE)

DE CHROMOCOR XII RENDIME PRAME ORF TLLO42C.

DE CHROMOCOR XII RENDIME PRAME ORF TLLO42C.

SECCHANOTICS CREWTISTAE (RAST) PAST)

CEDARTOTA, FUNG; ASCONTCOTINA; HEMIASCONTCETES.

RE 101

RE SEQUENCE PROM N.A.

RE SEGUENCE PROM N.A.

RE SEGUENCE PROM N.A.

RE SEGUENCE PROM N.A.

RE SEGUENCE PROM N.A.

SEGUENCE 167 AA: 19759 MM; 5AB8F574 CRC32;

Query Match 0.7%; Best Local Similarity 100.0%; Matches 7; Conservative Score 7; DB 3; Length 167; Pred. No. 1.01e+01; 0; Mismatches 0; Indels 0 Caps

0

36 DGLLLRL 42 ||||||| |892 DGLLLRL 888

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PRELIMINARY; PRT; 169 AA

RESULT 39 ID 001388

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Page 53

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Page 54

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                                                                      Query Match 0.7%;
Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SULT 43
Q36935; PRELIMINARY;
Q36935; CTREMBLREL(
Q1-NOV-1996 (TREMBLREL(
Q1-NOV-1996 (TREMBLREL(
TOPK,
TOPK,
                                                                                                                                                                                              SECUENCE FROM N.A., KERLAVAGE A.R., FLEISCHMANN R.D.;
HHITE D., CLAYTON R.A., KERLAVAGE A.R., FLEISCHMANN R.D.;
SEMBLITZED (SEP-1996) TO DEL/GENBANK/DDBJ DATA BANKS.
EMBL. U33841; G1544515; - G15445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 09:28:25 1998
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||||||||
251 SRSLPLP 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SENDIRACE FROM N.A.

ROSENBLATT:
ROSENBLAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SECURACE FROM N.A.

REDLINE: 8231-8449.

SHIMOTONIO X., TAKANASHI Y., SHIMIZU N., GOJOBORI T.,

REDLINE: 8231-8449.

REDLINE: S. HIFM. N., SUGLMUBA T.;

PROC. NATL. ACAD. SCI. U.S.A. 82:3101-3105(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SECUENCE FROM N.A.
MEDILINE: 8425019
SCHEMENT, PARNCA R., PERKINS D., BRIGGS D., LEE T.H.,
COLIGAN U., PONG-STAML F., GALLD R.C., BASELTINE W.A.;
SCHEME 235-41-424(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TERSINA PERDOPUBERCUOSIS.
PLASHID PIB.
PROMATOTA; GENCILICUTES; SCOTOBACTERIA; PACULTATIVELY ARAEROBIC RODS;
ENTEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VIRIDAE: SS-RA, NONENYELOPED VIRUSES; POSITIVE STRAND RAA VIRUSES;
RETROVIRIDAE; ONCOVIRINAE: TYPE C ONCOVIRUS GROUP;
NAMMALIAN TYPE C ONCOVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEOURNCE FROM H.A.

WEISS R.L., TEICH H., VARHUS H., COPPIN J.;

(IN) WEISS R.L., TEICH H., VARHUS H., COPPIN J.;

REAL TUNON VIEWES; SECOND FUITION J., VOL. 2.1070-1085;

COLD SPRING HARBOR LABORATORY, COLD SPRING HARBOR (1985).
          70 TPLRTLV 76
                                                                                                                                                                                                                                                                                                                                                                                                                        EXECUTION R.D., ADMAS M.D., HRITE O., CLATTON R.A., KIRKHESS R.P.,
FERMYZ K., FORGERT D.A., LEREN D.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PÓURICE FROM N.A.
TATUSOV R., MUSHECIAN A.R., BORK P., BROWN N.P.,
DRODOVSKY M., RUDD K.E., KOONIN E.V.,
TRR. BIOL. 6:279-291(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOLINCE FROM N. DAMES H. D., WHITE O., CLAYTON R.A., KIRKNESS R.F., ELSCHMANN R.D., ADAMS H.D., WHITE O., CLAYTON R.A., KIRKNESS R.F., DELSCHMANN R.D., ADAMS H.D., WHITE O., CLAYTON R.A., KERKLEN J.H., ENGLES C.A., CANTER J.D., KIRKLEY J.K., STENDER B., LIU L.I., GLODER A., KELLEY J.K., WEIDMAN J.F., TILLIPS C.A., CONTEGNACK T.R., SHILLIPS D.T., SANDEK D.H., BRANDON R.C., FIRE L.D., LICHTONALD L.A., SHRILLE D.T., SANDEK D.H., BRANDON R.C., FIRE L.D., TORNALL K.V., FORSHICE H.S., GNEEN C.L., DANIEL B. A., SANDEN C. L.D., SHILLIPS D.C.; FIRE L.D., TENDER D.H., SANDEN C. S., GNEEN C.L., D., SHILLIPS D.C.; FIRE L.D., VENTER J.C.; JENCE 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -FEB-1997 (TREMBLREL.
-FEB-1997 (TREMBLREL.
-AUG-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTIEDICAL.
1683:
BADOHIUS INFLUENSAE.
BANCHICA: GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
STEDERLIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       222
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Pred. No. 1.01e+01;
0; Mismatches 0; Indels
                                                                            Score 7; DB 2; Leng
Pred. No. 1.01e+01;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                                                                                                                                        Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAYES W.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GOLDE D.W.
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                5 B
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OGASAWARA N.;
SUBMITTED (APR-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EQUENCE FROM N.A.
STRAIN=168;
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EMBL/GENBANK/DDBJ DATA

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RESULT 44

DREIMINARY: PRT: 182 AA.

DO 668704

DO 7000

DO
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Best Local Similarity 100.0%;
Matches 7; Conservative
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005503 PRELIMINARY;
005503;
005503;
01-7UL-1997 (TREMBLREL.)
01-7UN-1997 (TREMBLREL.)
01-7UN-1998 (TREMBLREL.)
01-7UN-1998 (TREMBLREL.)
VENUE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLASMID. PLASMID NA: 21000 MM; ADB431D7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 GSILSTL 68
|||||||
856 GSILSTL 862
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||||||||
856 GSILSTL 862
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE PROM N.A.
STRAIM-RIM:
HU P., ELLIOTT J., MCCREADY P., SKOWRONSKI E.; GARNES J.,
HU P., ELLIOTT J., MCCREADY A.V., BRUDAKER R., CARCIA E.;
KORAKASHI A., CARCANO A.V., BRUDAKER R., CARCIA E.;
SUBMITTED (MATTED) (
                                                                                                                                                                                                SEOURICE FROM N.A.
STEALM-16: A. FASANIA N., SAGAI H., ITAYA N., KASANARA
A. N. TAYA K., FUJITA M., SAGAI H., ITAYA M., KASANARA
A. N. TAYA M. PUJITA M., SAGAI H., ITAYA M., KASANARA
A. N. TAYA M. PUJITA M., SAGAI H., ITAYA M., KASANARA
A. N. TAYA M. TAYA M. TAYA M. TAYA M. TAYA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    904 TFLRTLV 910
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PLASMID PODI.
RROMANIOTA: GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC
RROMANIOTA: GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC
RIVEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
HOLMSTRYM A.H.;
SUBMITTED (DEC-1994) TO EMBL/GENBANK/DDBJ DATA
EMBL, D18804; G619941; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REDILIEE: 95286274.
HOLMSTROM A., ROSQVIST R., WOLF-WATE H., PORSBERG A.;
INPECT. IMMUN. 61:2269-2276(1995).
DODENCE FROM N.A.
TRAIN-168;
ADAIE Y., YATA K., FUJITA M., SAGAI H., ITAYA M., KASAMARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCILLOS SUBTILIS.
ROKARYOTA; FIRMICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 7; DB 2; Length 182;
Pred. No. 1.01e+01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C744A6PD CRC32;
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RESULT OF STANDARD ST
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DESCRIPTION OF PRELIMINARY; PRT: 206 AA.
AD 201550.
DT 01-MS-1996 (TREDBLEEL. 01. CREATED)
DT 01-LAW-1996 (TREDBLEEL. 05. LAST REQUERCE UPDATE)
DT 01-LAW-1998 (TREDBLEEL. 05. LAST REQUERCE UPDATE)
DT 01-LOC-1998 (TREDBLEEL. 05. LAST RECORTION UPDATE)
DE REPORTECTION FROTEIN CAICA-8 (FRANCENT).

CAICA-1998 (TREDBLEEL. 05. LAST RECORTION OF CREATER TEAL
CONTROLLABORITIS ELECAMS.

CE EURANCOTA- RECORDAN ACCELORATES NEMATODA: SECERMENTEA.
RESURVEY FROM N.A.
RA WILSON R. AINSCOUGH R., ANDERSON K. BAYRES C. BERKS
RA LIBERT J. LAISTER N. LASTELLE P. TOLFRYNIG J. LLO
RAM KIRST J. HILLER L. JIER M. JOHRSON J. LAISTON A. CHESTER N. LASTELLE P. LORRING J. LLO
RAM KIRSTEN J. LAISTEN R. PARELLE P. LORRING J. LLO
RAM KIRSTEN J. LAISTEN R. LASTELLE P. LORRING J. LLO
RAM KIRSTEN J. LAISTEN R. LASTELLE P. LORRING J. LLO
RAM KIRSTEN J. LAISTEN R. LASTELLE P. LORRING J. LLO
RAM KIRSTEN J. LAISTEN R. LASTELLE P. SEMALO
RAM KIRSTEN J. LAISTEN R. LASTELLE P. SEMALO
RAM KIRSTEN J. LAISTEN R. LASTELLE P. LORRING R. SEMENTARY R. LASTELLE P. LORRING R. SEMENTARY R. LASTELLE P. LASTELLE P. LORRING R. SEMENTARY R. LASTELLE P. LORRING R. SEMENTARY R. LASTELLE P. LASTELL
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MOB
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                                                                                                                                                                                                                                                Query Match 0.7%;
Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%; Pred. Mo. 1.01e+0;
Matches 7; Conservative 0; Mismatches 0; Indels
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950447 PRELIMINARY;

050447;

01-NOV-1996 (TREMBLREL 01, C

01-XNN-1998 (TREMBLREL 05, I

01-UN-1998 (TREMBLREL 06, I
110 KELVARV 116
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100 KELVARV 106
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735 VTGAYDT 741
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JERRIC V.
JERRIC V.
JERCIRIOL. 178:3314-3321(1996).
ZEGL: 035121: 8314479; --
ZEGL: 0101711 6509815; --
ZEGL: 010171 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-168;
KINST F., COLSANANA, N., YOSHITANA, N., DANCHIN A.;
SURMITTED (NOW-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL, DBBB03; D1004691 ...
EMBL, 1991007; E11012559 ...
SEQUENCE 205 AA; 22536 MM; 61C1E275 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SERROR P., SHIW B.S., SOLDO B., SOROKIN A., TACCONI E., TAKAGI T.,
TAKAHASHI H., TAKEMAN K., TAKECHI H., TAKAGSHI A., TAWAKA T.,
TERSPIRA P., TOGRONI A., TOSATO V., UCHILMAS Y., VANDESDI M.,
VANNUER F., VASSATOTI A., VIARI A., WANDUTT R., WEDLER E., WEDLER R.,
WEITLENSGER T., MINTERS P., WIRAT A., TAWAMOND H., TAWAHE K.,
TAGMOND K., TATA K., TOSHIMA K., TOSHIKAWA H.F., EDMSTRIN E.,
TOSHIKAWA H., DANCHIM A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TEALWHISTRY.
TEDLINE: 96236050.
TAR L.E., CURCIC R., MUDD M.H., DHANDAYUTHAPANI S., GLMER R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQUENCE FROM N.A.
TRAIN=H37RV;
ADCOCK K., CHURCHEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STOURNET PROM N. ANDERSON K. BAYRES C., BERKS M., BOWFIELD J., UNTON J., CONNELL M. COPERT J., COOPER J., COULSON M. CRAYON M. M. LOTON T., CONTROL M. COPERT J., COOPER J., CARDNER M., CREEN M. A., GREEN P., MARINS T., HILLIER L., JIER M., JOHNSTN L., JOHES M., KERSHN J., LATON C., LISTEN J., LATERIAL P., LIGHTMING J., LLOTD C., TOURRAY J., LATON C., COURRAY J., MORTHORE B., O'CHLAGHAN M., PASSON J., PERCY C., LIKEN L., ROPERA N., SAUDERS D., SHONKEEN R., SALLON M., SMITH A., ROURHAMER R., STANDAN R., STUSTON J., THOMAS K., ANDIN M., MATSON A., MATSON A., MATSON CA., MATSON C., MATSON CA., MATSON CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOUZNCE FROM N.A.
TRAIN-MAJYRY:
TRAIN-MAJYRY
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Urton J.;
Urmitted (Jah-1995) to engl/genbank/ddbJ data banks
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KARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DCOCK K., CHURCHER C.M.;
PMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COBACTERIUM TUBERCULOSIS.
OKARYOTA: FIRMICUTES; ACTINOMYCETALES; MYCOBACTERIACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LE S.T., BARRELL B.G., RAJANDREAM M.A.;
BAITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DENCE OF 4-228 FROM N.A.
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                                                                                                                                                                                                                                                Score 7; DB 2; Length 228; Pred. No. 1.01e+01; O; Mismatches O; Indels
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Search completed: Fri Dec 18 18:47:31 1998 Job time : 205 secs.

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Dec 21 09:28:25 1998
                                                                                                                                       Query Match 0.7%; Score 7; DB 2; L
Best Local Similarity 100.0%; Pred. No. 1.01e+01
Matches 7; Conservative 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 1.01e+01;
Matches 7; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.01+c1);
Matches 7; Conservative 0; Mismatches 0; Indels
147 REAGVPL 153
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230 REAGVPL 236
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69 FRALVAQ 75
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|||||||
827 LPDVPLR 833
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WATURE 368:12-36(1994).
EMBL: #48045: #1414246: -
HYDOTHERICAL PROTEIN.
NON_TER 206 206
SEQUENCE 206 AA; 23256 MM; ODF4EDIE CRC32;
                                                                                                                                                                                                                                                             NON_TER 1 1 SEQUENCE 231 AA; 24338 MW; 0529956C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               069113 PRELIMENTY PRT. 231 AM.
069113 PRELIMENTY PRT. 231 AM.
069113 PRT. 231 AM.
069115 PRT. 231 AM.
06916 PREMBLEEL O7. CREATE
01.AUC-1998 (TREMBLEEL O7. LAST SEQUENCE UPDATE)
01.AUC-1998 (TREMBLEEL O7. LAST SMOTATION UPDATE)
01.AUC-1998 (TREMBLEEL O7. LAST SMOTATION UPDATE)
020ATURE DIFFUNCATION UPDATES
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                                                                                                                                                                                                                                                                                                                                            SENCUENCE FROM N.A.

STRAIN-10265.

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EUBACTERIA: PROTEOBACTERIA; BETA SUBDIVISION; BURKHOLDERIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                      Length 231;
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252 6 0.5 287 8 R44511 Rat type I Lodothyron 5.54e+02 255 6 0.5 280 1 R87652 Helicobacter pylori a 5.54e+02 255 6 0.5 280 280 280 280 280 280 280 280 280 280	Mon Dec 21 09:28:26 1998 US-08-951-733-20.rag	Staphylokinase deriva S. See-02	Mon Dec 21 09:28:26 1998 US-08-951-733-20.rag
	Page 7		Page 5
5. Schenophilus emophilus	Hon Dec 21 09:28:26 1998 US-08-951-733-20.rag	### REPRESENTATION OF THE PROPERTY OF THE PROP	Mon Dec 21 09:28:26 1998 US-08-951-733-20.rag

6 0.5 487 3 R13596 Di dopamine receptor.	## 155	Mon Dec 21 09:28:26 1998 US-08-951-733-20.rag	### Second State	Mon Dec 21 09:28:26 1998 US-08-951-733-20.zeg	
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6 0.5 522 2 970554 HIV virus gas gene.	507 6 0.5 487 71 W0775 508 6 0.5 489 71 W0775 508 6 0.5 490 77 R8936 509 6 0.5 490 77 R8936 500 6 0.5 490 78 R8938 500 6 0.5 490 78 R8938 501 6 0.5 490 78 R8938 502 6 0.5 491 78 R8938 503 6 0.5 491 78 R8938 503 6 0.5 491 78 R8938 504 6 0.5 491 78 R8938 505 6 0.5 491 78 R8938 506 6 0.5 491 78 R8938 507 78 R8938 508 6 0.5 497 78 R8938 509 6 0.5 497 78 R8938 500 78	Mon Dec 21 09:28:26 1998 U9-08-951-733-20.rag	### According to the control of the	Mon Dec 21 09:28:26 1998 US-08-951-733-20.reg	

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711 6 0.5 1116 7 R15156 712 0.5 1117 3 R15157 713 1 0.5 1118 3 R15157 714 6 0.5 1118 28 W43991 715 6 0.5 1118 28 W43991 716 6 0.5 1118 28 W43991 717 6 0.5 1118 28 W43991 718 6 0.5 1118 28 W43991 719 6 0.5 1218 20 W10688 719 6 0.5 1218 20 W10688 719 6 0.5 1218 20 W10688 719 6 0.5 1218 21 W11587 710 6 0.5 1218 21 W11587 711 6 0.5 1218 21 W11587 712 6 0.5 1218 21 W11587 713 6 0.5 1218 21 W11587 714 6 0.5 1218 21 W11587 715 6 0.5 1218 21 W11587 717 6 0.5 1218 21 W11587 718 6 0.5 1218 12 R65011 718 718 718 718 718 718 718 718 718 718	Mon Dec 21 09:28:26 1998 US-08-951-733-20.zag	### Properties	Mon Dec 21 09:28:26 1998 US-08-951-733-20.zag

0.4 465 13 R66758 Anti-tobacco mossic v 4.8	### 1864 5 0.4 321 16 R90771 Bacillus stearothermo .03e403 ### 1865 5 0.4 321 5 R25591 Recombinant hematopoi .03e403 ### 1866 5 0.4 327 16 R8973 Recombinant hematopoi .03e403 ### 1866 5 0.4 327 16 R8973 Gryprotein coupled hum .03e403 ### 1867 5 0.4 327 16 R8973 Gryprotein coupled hum .03e403 ### 1871 5 0.4 321 18 R8732 Gryprotein coupled hum .03e403 ### 1871 5 0.4 324 R87132 Gryprotein coupled hum .03e403 ### 1871 5 0.4 324 R87132 Gryprotein coupled hum .03e403 ### 1871 5 0.4 324 R87132 Gryprium cinterum per .03e403 ### 1871 5 0.4 324 R87132 Gryprium cinterum per .03e403 ### 1871 5 0.4 324 R87132 Gryprium cinterum per .03e403 ### 1871 5 0.4 324 R87132 Gryprium cinterum per .03e403 ### 1871 5 0.4 324 R87132 Gryprium cinterum per .03e403 ### 1872 6 0.4 324 R87132 Gryprium cinterum per .03e403 ### 1872 6 0.4 324 R87132 Gryprium cinterum per .03e403 ### 1873 6 0.4 324 R87132 Gryprium cinterum per .03e403 ### 1873 6 0.4 324 R87132 Gryprium cinterum per .03e403 ### 1873 6 0.4 324 R87132 Gryprium per .03e403 ### 1873 6 0.4 324 R87132 Gryprium per .03e403 ### 1873 6 0.4 324 R87132 Gryprium per .03e403 ### 1873 6 0.4 324 R87132 Gryprium per .03e403 ### 1873 6 0.4 324 R87132 Gryprium per .03e403 ### 1873 6 0.4 424 R87132 Gryprium per .03e403 ### 1873 6 0.4 425 R87132 Gryprium per .03e403 ### 1873 6 0.4 425 R87132 Gryprium per .03e403 ### 1873 6 0.4 425 R87132 Gryprium per .03e403 ### 1873 6 0.4 425 R87132 Gryprium per .03e403 ### 1873 6 0.4 425 R87132 Gryprium per .03e403 ### 1873 6 0.4 425 R87132 Gryprium per .03e403 ### 1873 6 0.4 425 R87132 Gryprium per .03e403 ### 1873 6 0.4 425 R87132 Gryprium per .03e403 ### 1873 6 0.4 425 R87132 Gryprium per .03e403 ### 1873 6 0.4 425 R87132 Gryprium per .03e403 ### 1873 6 0.4 425 R87132 Gryprium per .03e403 ### 1873 6 0.4 42	Mon Dec 21 09:18:26 1998 US-08-951-733-20.reg	### State	Mon Dec 21 09:28:26 1998 US-08-951-733-20.xeg
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5 0.4 601 8 R43348 Human GFAT.	### State	Kon Dec 21 09:28:26 1998 US-08-951-733-20.rag	### RAIDES RAIDES RAIMAN Total reactive Raides Raides	Non Dec 21 09:28:26 1998 US-D8-951-733-20.rag

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2 18-7AN-1992. 164548.
2 21-UN-1992. 3P-164548.
2 18-1992. 3P-164548.
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R4574;
R4574;
Byolnositol delydrogename:
Transformant; myolnositol delydrogename:
coli; substrate specificity; Bacilium.
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W03397; standard; Protein; 296 AA.
W03397; 19-PEB-1998 ((irst entry)
Ruman clone 55 protein.
Src-bamology region 3 domain; human; mouse; 8H3 domain; cell growth; cellular signaling element; cellular structural element; malignancy; protein identification; functional domain; protein screening; scan sapiens.
W00831635-A1.
U-0-07-1956:
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251 SRSLPLP 257
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nothelmintic.
Saccharopolyspora erythraea.
209723630-42.
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Pred. No. 4.52e+01;
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Page 28

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Query Match 0.6%; Best Local Similarity 100.0%; Matches 7; Conservative

Score 7; DB 11; Length 354; Pred. No. 4.52e+01; 0; Mismatches 0; Indels

RESULT 6

RE 23912:
AC RE3931;
AC RE3931;
BT 21-FE3-1995 ((irst entry))
E Interlewkin 8 (IL-8) receptor:
An Interlewkin 8 (IL-8) receptor:
AN Interlewkin; receptor antinfiammatory; psoriasis; reperfusion;
AN Interlewkin; receptor antinfiammatory; psoriasis; reperfusion;
AN Interlewkin; receptor antinfiammatory properties
BY 17-WK-1991; DF-149245.
BY 17-W

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PP 04-APR-1986; U04454.

PR 03-APR-1986; U5-630115.

PR 03-APR-1986; U5-630115.

PR 03-APR-1986; U5-630115.

PR 03-APR-1986; U5-630115.

PR 10-APR-1986; U5-630115.

PR 10
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98 atslega 104
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304 ATSLEGA 310
                                                                                                                                                                                                                               gene - for production and engineering of myoinositol dehydrogenase claim 3: Page 8-9: 13pp; Japanese. Claim 3: Page 8-9: 13pp; Japanese. The sequence (Q55708) shows a recombinant plasmid which encodes myoinositol dehydrogenase. The plasmid can be transformed into a mitable host thus producing myoinositol dehydrogenase quickly a mitable host thus producing myoinositol dehydrogenase quickly.
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W19715 sandard; Protein; 333 AA.
W19715;
18-SEP-1997 (first entry)
Sugar biosymthesia entyma ErgBII;
Polyketide; glycosylation; ergBII; L-mycarose; antimicrobial;
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|1141 ANPALPS 1147
                                                                                                                                                                                        Sequence 334 AA;
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Pred. No. 4.52e+01;
0; Mismatches 0; Indels
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     RESULT 12

WO3315 tandard; Protein; 358 AA.

WO3316 tandard; Protein; 358 AA.

WO3316 tandard; Protein; CR3.

WO 11.0487-1997 (first entry)

RE Human cytokine response protein CR3.

WW 154and stimulated gene expression; diagnosis; therapy;

WW signal transduction.

WW 164and spiens.

WW 164and spi
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12 (31 PM, Reagon JW, Moodward DF;

13 (41 PM, Reagon JW, Moodward DF;

15 (41 PM, Reagon JW, Moodward DF;

16 (42 PM, Responding human HP4 prostaglandin receptor - useful for drug

17 providing human HP4 prostaglandin receptor.

17 contenting an Experience of the prostaglandin receptor.

17 transfected cellar contenting an HP4 prostaglandin receptor.

18 pression vector, can be used to screen for substances that

19 contenting an HP4 prostaglandin receptor to the HP4 receptor, and too EP64 receptor spondure

19 binding to the HP4 receptor, and for HP4 preceptor spondure

19 (based on increased cAMP production in cells pretreated with a

19 prosphedienterase inhibitor).
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Best Local Similarity 100.0%;
Matches 7; Conservative
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241 PGARRRG 247
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RABZIZ: standard; Protein; 355 AA.
RABZIZ;
04.ADR-1993 (first entry)
Sequence in a high affinity recombinant rabbit interleukin-8
(II-8) receptor polypeptide in FBR.
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1104 LTRHRVT 1110
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Similarity 100.0%;
7; Conservative
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0; 1
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Pred. No. 4.52e+01:
0: Mismatches 0: Indels
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. No. 4.52e+01;
Mismatches 0; Indels
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the CR coding region
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RESULT:

13 DR 2569; atandard; Protein; 375 AA.

No w2569; atandard; Protein; 375 AA.

No w2569; atandard; Protein; 375 AA.

No w2569; atandard; protein; atandard; protein; atandard; human.

No w2569; atandard; protein; atandard; protein; atandard; human.

No w2569; atandard; protein; atandard; human.

No w2569; atandard; protein; atandard; human.

No w2569; atandard; atandard; human.

No w2569; atandard; human xidney potessium ion channel - and protein; atandard; atandar
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ID #44346;
AC #44346;
DY 15-MAY-1996 (first entry)
DE Buman HPA prostaglandin receptor:
KW Human; HPA prostaglandin receptor: a
KW GAMP.
OS Homo sapiens.
PM US5716835-A.
PM US5716835-A.
PM 05-MAY-1994; US-239431.
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Best Local Similarity 100.0%;
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1104 LTRHRVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genes (see also 74376-8) isolated from a thiol-selected interleukin 2-indused human T-cell blaat cDMs library. 6 Genes (CRL, 2. 3, 5, 6, 8) are novel. CR3 shows homology to G-coupled 7 transmenbrane spanning receptors of the prostagiandin family and probably plays a regulatory role in cellular proliferation and/or inflammation. It provides a novel receptor that allows the manipulation of cellular functions controlled by blochemical pathways signalled by the receptor and may be used to identify lignals useful for modulating cellular proliferation and inflammation. Recombinant CR3 polypeptides can be produced in bost sequence 338 As.
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cyclase;

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US-08-951-733-20.rag

Page 32 Score 7; DB 6; Length Pred. No. 4.52e+01; 0; Mismatches 0; In

Indels 355;

0 Caps

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Pred.

re 7; DB 20; Lens d. No. 4.52e+01; Mismatches 0;

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RESULT 17
ID W24252 standard; Protein;
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| 260 PRRGAAP 266
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| 260 prrgaap
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Pred. No. 4.52e+01
0; Mismatches
                                                                                                                                                                                                                                                                        Score 7; DB 3; Length 395;
Pred. No. 4.52e+01;
O; Mismatches 0; Indels
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Pred. No. 4.52e+01;
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RA1330 standard; Protein; 395 AA.

RA1330 standard; Protein; 394 Actobinase; 394 Acto
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W09729197-A1.

PD 14-NG-1997.

PP 21-JNN-1997.

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Ph 207-SPE-1986: 934705.

PR 207-SPE-1986: 934705.

PR 20-PRE-1986: 934705.

PR 20-PRE-1986: 934705.

PR 20-PRE-1987: 935-96439.

PR 20-PRE-1997: US-967949.

PR 20-PRE-1997.

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     D 88807 standard; Protein; 429 AA.

R88407, 6 (first entry)

Beta-(1.6)-endoglucanase;
W Trichoderma harzianum beta-(1.6)-endoglucanase; Am

Peta-glucan degradation; pustulanase.

Trichoderma harzianum.

WD952133-AL.

21-807-1895.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%;
Matches 7; Conservative
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|||||||
437 LRAAVTP 443
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18-PER-1908 (first entry)
18-PER-1908 (first entry)
Ammonitex degensii appartate aminotransferase; K4/AA; chiral compound.
Ammonitex degensii strain KC4.
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260 PRRGAAP 266
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Pred. No. 4.52e+01;
0; Mismatches 0;
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Production of very long chain fatty acid(s) in plant(s) - to produce drought and stream resistant transgenic plant(s) - to produce drought and stream resistant transgenic plant(s) - to produce produce drought and stream resistant and stream resistant application mo 9,1012A1, Jojoba fatty acyl reductase sequence is known a membrane preps. having wax synthase activity is solutted, the wax synthase activity is solutiled, and the wax synthase activity is solutiled. The source material is the outer shells and seed coats of jojoba embryos.
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Dish construct expressing jojobs wax synthase and transformed Brassica cells: - useful for producing wax ester(s) for use in pharmaceuticals and commercies, etc.

Disclosure; Column 43-46; 50pp; English.

A jojobs fatty-acyl-reductase CORN was used in the construction of vectors for plants ransformation. Transgenic plants, e.g. cliseed rape, expressing the reductase in addition to a heterologous sequence 433 As;
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Query Match 0.6%; Best Local Similarity 100.0%; Matches 7; Conservative Score 7; DB 14; Length 493; Pred. No. 4.52e+01; 0; Mismatches 0; Indels 0; Caps

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€ ₽ 426 lllrlvd 432 ||||||| 884 LLLRLVD 890

BSULT 24

Day 165: standard: Protein: 493 AA.

C 81765: 1993 (first entry)
20 -8EP:1993 (first entry)
20 -8EP:1993 (first entry)
21 -920-bas wax synthase ensyme.

RM fatty acyl reductase: jojoba: wax exter; wax synthase; connectas;
RM fatty acyl reductase: jojoba: wax ester; wax synthase; connectas;
RM detargents: plastica; jojoba: wax ester; wax synthase; connectas;
RM detargents: plastica; jojoba: wax ester; wax synthase; connectas;
RM detargents: plastica; jojoba: wax ester; wax synthase; connectas;
RM detargents: plastica; jojoba; wax ester; wax ester; wax ester; wax ester; while.
PM R01-1091: US-786216.
PM 10-1091: US-786216.
PM 1

RR CORRESPONDENCE COSSION COSS pr Laxisabal ND, Lassner NM, Meta JG;

DR WF. 99.18256/23.

DR WF. 99.18256/24.

DR WF. 99.18256/25.

Pr produce vax ester(s) - comprises nucleic acid acquarce which

Pr produce vax ester(s) - comprises nucleic acid acquarce which

Pr sequence not naturally associated with wax synthase protein

Pr sequence not naturally associated with wax synthase protein

Pr sequence given in R37455-66 represent the jojoba wax synthase

CC Trick acquarce given in R37455-66 represent the jojoba wax synthase

CC (fatty acylifetty alcohol Apyltransferses) and fatty acyl reductase

CC (fatty acylifetty alcohol Apyltransferses) and fatty acyl reductase

CC a construct in which the wax synthase gene is associated with a

CC a construct may be used to produce crop plants having a convenient

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CC construct may be use

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/note= "calmodulin-binding domain"
339..517
/note= "visinin-like domain"

PR 189735968-AL.

PN 189735968-AL.

PN 20-OCT-1997. UD5156.

PP 27-MAR-1997. UD5156.

PP 27-MAR-1997. UD5156.

PP 27-MAR-1996. US-655332.

PR 28-MAR-1996. US-655332.

PR 28-MAR-1996. US-655332.

PR 28-MAR-1996. US-65332.

PR 28-MAR-1996. US-6747.

PR 28-MAR-1996. US-6747.

PR 28-MAR-1996. US-6747.

PR 28-MAR-1996. US-78-MAR-1996.

PR 28-MAR-1996. US-78-MAR-1996

Query Match 0.6%; Best Local Similarity 100.0%; Matches 7; Conservative Score 7; DB 27; Ler Pred. No. 4.52e+01; 0; Mismatches 0; Length 517; 0 Cape

511 leslrps 517 |||||||| 369 LSSLRPS 375

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26
190919 standard: Protein; 517 AA.
190919 (first entry)
Tobacco calcium/calmodulin-dependent protein kinase.
Calcium/calmodulin-dependent protein kinase male aterile plant;
Calcium/calmodulin-dependent protein kinase male aterile plant;
Ricotiana thems hybrid plant; cobacco; CCaKK; transgenic plant.
Ricotiana thems SRI.
Ricotiana thems SRI.
Romain 300.335
Commain "----"" "Almodulin-binding domain"

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standard; protein; 834

I-1990 (first entry)
-1-6-glucanase.
roides thetaiotamicron;
roides thetaiotamicron K ; alpha-1-6-glucanase; KHM098. dental

caries;

f dental caries. scale prodn. of

large scale prodn is useful for the

601 mrpifle 607 ||||||| 411 MRPLFLE 417

834;

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970347. 18-MAY-1991 (first entry) Varicella-zoster virus (VSV) immunogenic outer surface protein. Varicella-zoster virus: gB gene product; varicella: Vaccine. EP-310931-A.

DESCRIPT 28

ID 970347;

AC 970347;

AC 970347;

DT 18-MAY-1991 (first entry)

DE Varicella-roster virus (VSV) immuno;

EW Varicella-roster virus (SSV)

EW Varicella-roster virus (SSV)

EW 12-00-1987;

PD 1 Davison ž

Pragment of varicella-soster virus - used for producing poly:peptide for use as vaccine against VEV disease and pox: Claim 2; Page 25-28; 29pp; English. The protein sequence encodes an immunogenic outer surface VZV protein chicken

Dec 21 09:28:26 1998

Page 41

Kon

UB-08-951-733-20.rag

Page 42

detergents, plastics and lubricants. Production of wax esters in crop plants allows easier isolation than from traditional sources, eg. jojoba and sperm whale.

Sequence 493 AA;

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Query Match 0.6%; Best Local Similarity 100.0%; Matches 7; Conservative Score 7: DB 7: Length 493; Pred. No. 4.52e+01; 0; Mismatches 0; Indels 0

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\$ B 426 lllrlvd 432 |||||| 884 LLLRLVD 890

standard; Protein; 493

R87509 stand. R87509; 15-0CT-1995

15-OCT-1995 (first entry)
Resynthesised jojoba fatty-acyl-reductase.
Uojoba, fatty-acyl-reductase; ensyme; transgenic plant;
Brassics:

simmondeia chinensis. WO9533055-A2. 07-DEC-100"

ID SSULT TO DE LOS OF MELT OF SELECTION OF S

pp 07-082-1995: U06671.
pp 01-7UN-1996: U0-251464.
pp 01-7UN-1996: U0-25146.
pp 10-7UN-1996: U0-25146.
pp 10-7UN-1996: U0-25146.
pp 10-7UN-1996: U0-25146.
pp 10-7UN-1996: U0-7UN-1996: U0-7UN-1996

Query Ma Best Loc Matches O.6%; Local Similarity 100.0%; tes 7; Conservative Score 7; DB 18; Length Pred. No. 4.52e+01; O; Mismatches O; Ind Indels 0 Gaps

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문 426 lllrlvd 432 ||||||| 884 LLLRLVD 890

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US-08-951-733-20.rag

Page 45

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which is used in the p
disease, varicella. 1
VZV antibody titers.
Sequence 854 AA;
                              preparation
The antigen
                              of a vaccine is also used
                              to protect against ZVE in the diagnosis of
```

문 Query Match 0.6%; Best Local Similarity 100.0%; Matches 7; Conservative Score 7; DB 2; Length Pred. No. 4.52e+01; 0; Mismatches 0; In 854; 0

> Gaps 0

Ś 287 lytphit 293 |||||||| 894 LYTPHLT 900

RESULT 29

RESULT 393 (first entry)

RESULT 394 (first entry)

RESULT 395 (first entry)

RESULT

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THE RESERVE TO SOLUTION OF THE PROPERTY OF THE

70 translation product HCMV UL70; screening;

DR SECULT

Homo sapines antivira.
GB3311068-A.
17-5EP-1997; 004575.
05-MAR-1997; 004575.
14-MAR-1995; US-007118.
14-MAR-1995; US-013189.
(MERI) MERCA 6CO INC.
GOLIN L. HARUMA DJ, LAfemina RI
MFI: 97-4473906/40.
P-PSDB; W27083.

Ouery Match 0.6%; Best Local Similarity 100.0%; Matches 7; Conservative Score 7; DB 26; Length 946; Pred. No. 4.52e+01; 0; Mismatches 0; Indels 0

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NULT 12 W27084 tandard; Protein; 946 AA. W27084.
18 *MR-1998 (first entry)
Ruman cytomegalovirus (RCWY)
Ruman cytomegalovirus halcose; RCM
Infection; diagnosis; antiviral.

397 slrtagt 403 |||||||| 1117 SLRTAGT 1123

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U8-08-951-733-20.

LO-MAR-1998 (first entry)
Ruman cytomegalovirus (RCMY) primase.
Human cytomegalovirus primase; HCMV, acreening; inhibitor; infection; diagnosis; da.
Homo aniens.
BEZZ11069-A.

pp 17-529-1997.

pp 01-MR-1997; 004577.

pp 04-MR-1997; 03-007317.

pp 14-MR-1996; US-01346.

pp (MERII) MERCEN 6 CO INC.

pr 06-tib L. Rasuda DJ. Lafemina RL;

pr 16-tib L. Rasuda DJ. Lafemina RL;

pr 18-tib 19-18-18073.

pr 18-pr 18-pr 18-pr 19-18073.

pr 18-pr 1

8

The Novel human cytomegalovirus helicase - used for screening for NCHV PT attivities and is dayosis a NCHV practice of the screen and is dayosis a NCHV practice of the present sequence represents human cytomegalovirus (RCHV) UL70 Ct than station product. The UL70 open reading frame spans nucleited as C 193035 through 100355 of HCHV AD169 which was amplified by PCR primers C 193735 through 100355 of HCHV AD169 which was amplified Moral and CC cloned into Med./Mani digested 19877H6 vector DNA to yield the plasmid CC p8877H6 UL70. The amplified HCHV UL70 orf sequence and it translational CC p8877H6 UL70. The amplified HCHV UL70 orf sequence and it translational CC product were determined. Recombination into BacPM 6 viral DNA, plaque CC purification and generation of viral stocks were by standard protocols. CC The protect pass used with a new HCHV belicase in a screening compounds which inhibit HCV helicase (preferably with an IC50 of not greater than 300Ms), and as a disponsatic tool for diseases squames 340 AM. Infaction.

Query Match 0.6%; Best Local Similarity 100.0%; Matches 7; Conservative Score 7; DB 26; Len Pred. No. 4.52e+01; 0; Mismatches 0; Length 946; 0

Gaps

0

片 397 slrtagt 403 |||||||| 1117 slrtagt 1123

RESULT TO SEE TO

IRSULY 3

BY 7665; standard; Protein; 966 AA.

BY 7665; ptandard; Protein; 966 AA.

BY 7665; ptandard; Protein; 966 AA.

BY 7665; ptandard; Protein; Protein; dentification; defect; alteration; RV stanatch spair; NSH; primer; identification; defect; alteration; RV stanatch spair; NSH; primer; identification; defect; alteration; RV endoc; tumour; vaccine.

BY 869514085-A2.

BY 869514085-A2.

BY 869514085-A2.

BY 11-007-1994; US-128910

BY 11-007-1994;

US-08-951-733-20.rag

Page 46

antiaers which neutralise vixal infectivity. The polypeptide or fragments of it are useful for the prepn. of vaccines or disposis of VPV infection.

Sequence 868 Ax;

Score 7; DB 4; Leng Pred. No. 4.52e+01; 0; Mismatches 0; Length 868; 0 Gaps

0,

Query Match 0.6%; Best Local Similarity 100.0%; Matches 7; Conservative

287 lvtphlt 293 ||||||| 894 LVTPHLT 900

B

01-AUG-1990 (first entry)
Phosphoenolpyruvate carboxylase
Phosphoenolpyruvate carboxylase;
Corypebacterium glutamicum.
Pp. 1884/D. 8 919 AA ; ppc; pTG1200; oxaloacetate;

O'Reagan

RESULT

ROSSLI2 standard: protein: 91

ROSSLI2 standard: protein: 92

ROSSLI2 standard: 92

ROSSLI2 standard: 92

ROSSLI2 standard: protein: 92

ROSSLI2 st pr 8.402-1989; GB-02119.

pr 8.402-1989; GB-02119.

nt 10263) Degrama AG.

10 Intel JP Lephach GD, Kalinovski J, Puhler A, O'Res

11 Viret JP, Lephage P, Lemoine Y;

nt PSDB; GOSA83.

nt PSDB; GOSA8.

pr 12 Deoxyribonucleic actic fragment, for L-amino acid
probed, from coryrebacterium glutanicum strain coding for

phosphoenolpyrwate carboxylass.

probed, in the control of the carboxylass.

Disclosures p. Emglish.

Educioures p. Emglish. for

the anaplerotic function of the cellit indirectly increases biosynthetic 0

Query Match 0.6%; Best Local Similarity 100.0%; Matches 7; Conservative Score 7; DB 1; Length 919; Pred. No. 4.52e+01; O; Mismatches O; Indels indels ö Gaps

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436 relseae 442 ||||||| 621 RELSEAE 627

RESULT 31 ID W27085 standard; Protein; AC W27085; 946

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compound and to Sequence 1366

o test drugs 6 AA;

for their effect on collagen metabolism

o,

Gaps

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RE R1702 standard; protein; 1366 AA.

RC R1702. 1995 (first entry)

RC Collagen Japha 1 (1) chain precursor.

RC R1702. 1995 (first entry)

RC Collagen Japha 2 (1) chain precursor.

RC Collagen Japha 3 (1) chain precursor.

RC Collagen Japha 4 (1) chain precursor.

RC Collagen Japha 1 (1) chain precursor.

RC Collagen Action Collagen RC Japha 1 (1) chain precursor.

RC Collagen Machael Street Collagen Street Collagen Machael Collagen Precursor.

RC Collagen Machael Collagen Machael Street Collagen Machael 
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By MySO(0173-14.

BY 1989: AUGS27,

BY 14-100-1989: AUGS28

BY 14-100-1989
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523 aklsigz 529
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pha-D-glucosyltransferase,
pha-D-glucosyltransferase,
pha-D-glucosyltransferase,
corser transferate plant; cloning Escherichis coll;
corser transferate plant; cloning Escherichis coll;
seg Lambds-cll, vector: plantid posiciol; plantid posiciol;
seg Lambds-cll, vector: plantid posiciol; plantid posiciol;
seg transferate con improvement planting carbohydrate; pasture;
sedstuff; seneence; deattent plantid food; pharmaceutical.
sedstuff; seneence; deattent plantid food; pharmaceutical.
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1047 standard; Protein; 1577
1047;
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Pred. No. 4.52e+01;
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Pred. No. 4.52e+01;
0; Mismatches C
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                                                                                                                                                                                                                                                                                   Length 1577;
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PR 10-589-1995; US-01374.

PR 14-899-1995; US-01374.

PR 14-8
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pp 11-SEP_1995; U14547.

pp 11-SEP_1995; U9-001744.

pp 10-SEP_1995; U9-001744.

pp 10-Man_1995; U9-001744.

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cc w07521-W07524, and W07527 represent T-cell modulating peptides that can ce be used in the method of the invention. These sequences are based on a cc portion of the generic peptide corresponding to residues 70-91 of the cally a complex (MEO) class I continue disease involving T-cell mediated destruction of tissue in cc antisen see W07520). The method is for affecting the course of an ic commania. These peptides are used especially to treat insulin dependent cd dabetes mellitus, preferably being administered during the pre-clinical cc stage to delay onset of the disease. Other diseases that can be treated care multiple scierosis, rheumatoid arthritis, provinsis, provinsis,
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pp 03-80V-1995, JP-25211.

pp 04-80V-1995, JP-25211.

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Blocksylated interleukin-8 15-mer peptide ligand 5.

W Bacteriophage peptide library; peptide epicope; therapeutic target;

W ariesated compound library; interleukin-8; II-8.

W wariesated compound library; interleukin-8; II-8.

W wariesated compound library; interleukin-8; II-8.

W worstalk-12.

PU M09735148-12.

PU M09735148-12.

PU M09735149-13.
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High High scandard; peptide; High scandard; hepatitis B; High protein fragment; High scattwiting factor inhibitor; therapy; High protein fragment; High scattwiting factor inhibitor; therapy; High scandard; hi
pp 23-MR-1997; 004176.

pp 21-MR-1996; US-622338.

pp 21-MR-1997; US-622338
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Best Local Similarity 100.0%;
Matches 6; Conservative
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67 AAFRAL 72
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252 RSLPLP 251
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Pred. No. 5.54e+02;
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WH 12560 standard; Peptide; 15 AA.

BO - APR: 1998 (first entry)

Biocitylated interleukin; 15 - mer peptide eptope; therapeutic target;

RW Hacteriphose peptide library; applide eptope; therapeutic target;

RW Hacteriphose peptide library; applide eptope; therapeutic target;

RW Hacteriphose peptide library; applide eptope; the same standard;

RW Hacteriphose peptide library; applide eptope; the same standard;

PR 12-MAR-1997; U04176.

RW HIL: 97-803157/44.

PR 12-MAR-1997; U04176.

PR 12-MAR-199
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Property (1972).

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Pred. No. 5.54e+02;
O; Mismatches 0; Indels
                                                                                            Score 6; DB 11;
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0; Mismatches
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365 PSFLLS 370

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w17555 standard; protein; 17 AA W17555;

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RESULT ID R7 AC R7 AC R7 AC R7 AC R7 AC H7 AC H7
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AND PART STATE THE PONDEY CIR: Test GEDA.

BY SOUTHERS.

PR 16-FEB-1996; UG 960299.

PR 16-FEB-1996; UG 960299.

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RT3314 standard; peptide; 20 AA.

C R74314; professional for the control of th
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Matches 6; Conservative
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365 PSFLLS 370
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Tax protein frequent; HTM'-1, human T-cell leuksemia virus; hepatitis B;
human lymphotropic virus; trans-activating factor inhibitor; therapy;
Tax-dependent transcription; viral infection; genetic disorder;
homorygous familial hypercholesterolaemia; cancer.
Busan lymphotropic virus.
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0; Mismatches 0; Indels
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Pred. No. 5.54e+02;
0; Mismatches 0;
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leukaemia;
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Promposition containing less antigen or microorganism that expresses proceed to treat or prevent catanate by reducing the level of prantibodies directed against less protein

Brample 4; Page 29; Jäpp: English.

CC This sequence is an internal fragment of human beta-92-crystallin. CI peptides constituting beta-92-crystallin verse synthesized and crespective oliopeptides. As a result, only peptide fragment amino conclusions are subjected to competitive inhibition assay of beta-92-crystallin. This suggests that the binding site (epitope) of the 92-crystallin. This suggests that the binding site (epitope) of the 92-crystallin or the antional was a result in the region (157-173).

Cans antigens of sequence of anino acide numbers 162-165 of beta-92-crystallin or a nicroorganism had can express a lens antigen are used in a pharmaceutical composition. The composition can be used to prepare can inhibitor of an incress of anti-lens protein anticodies. The composition that the composition and the content of the cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 49
ID W41212 standard; peptide;
AC W41212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dec 21 09:28:26 1998
                                                                                                                                                        Query Match
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WPI. 95-206307277.

WRV HTM-I antigenic peptide(s) - used for disgnosing HTM-I intection(s), partic. HTM-I associated myelopathy and adult T-cel leukemic.

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Beta-83-crystallin fragment (amino acids 85-101).
Beta-83-crystallin; lens protein; cataract; antigen; autoimmune;
epithelial cell; epitope.
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Bomo apiens.

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0; Mismatches 0;
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### Additional Company of the Compan	Non Dec 21 09:28:27 1998 US-08-951-733-20.xpr	### Color Co	Mon Dec 21 09:28:27 1998 US-08-951-733-20.xpx

**ROCESSION A60933 **ROLECUL_Typ Protein REFERENCE REFE	(EC 3.1.3.48) Ly-5 precursor CD45; PPPTY1; T-cell surface T-cell variant; 13-May-1988 text_change 1.13-May-1988 text_change 1.23-May-1988 text_change 1.23-May-1989 text_ch	RESULT A18314 * type complete EXTR: A18314 * type complete EXTR: A18314 * type complete A17328 *
Mon Dec 21 09:28:27 1998 US-08-951-733-20.rpr	US-08-951-733-20.xpx Page 23	Man Dec 21 09:28:27 1998
GENETICS CLASSIFICATION SECRETARILY leukocyte common antigen; leukocyte common pring of the pr	AFRC class III histono 5.47e+02 genome polyprotein 5.47e+02 glacing channels prote 5.47e+02 genome polyprotein 5.47e+02 genome polyprotein 5.47e+02 genome polyprotein 5.47e+02 aggreen previous 15.1 5.47e+02 aggreen previous 15.1 5.47e+02 aggreen previous 15.1 5.47e+02 aggreen previous 15.1 5.47e+02 calcium channel BI-1 5.47e+02 calcium channel BI-2 5.47e+02 calcium channel BI-3 5.47e+02 probablid membrane pro 5.47e+02 calcium channel BI-3 5.47e+02 genome polyprotein 5.47e+02 genome polyp	971 6 0.5 2142 2 B35099 MRC class III hitton 5.47e+02
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tocyte common antigen; leukocyte common (ic damain homology; e-phosphatase homology (ie phosphatase) homology common digramatigen; transmembrane protein; ic phosphatase NAI sequence *status predicted *label SIG\ Nocyte common antigen, 200% *status *label MAT Cksum 9727 '.S.; Shen, F.W.; Boyes, E.A. Sci. U.S.A. (1987) 84.5364-5368 Sf. S' exons in the specification of Ly-5 guishing hematopoietic cell lineages. 988) 28:271-277 es of Ly-5 glycoproteins of the mouse and other mammals. JOH ; NID:g198755; PID:g554185; GB:J04640; yer, C.M.; Pingel, J.T.; Thomas, M.L. 989) 264:5220-6229 tion in potential regulatory regions of the leukocyte common antigen gene. core 9; DB 2; Length 183; red. No. 1.20e-03; 0; Mismatches 0; Indels 0; Gaps 0; ocyte common antigen; leukocyte common ic domain homology; e-phosphatase homology fragment procursor - mouse (fragment) a specific) a specific musculus #common_name house mouse ence_revision 19-May-1989 #text_change core 9; DB 2; Length 24; red. No. 1.20e-03; 0; Mismatches 0; Indels 0; Gaps ocyte common antigen; leukocyte common ic domain homology; e-phosphatase homology abel RAS ; NID:g201105; PID:g201106 Sci. U.S.A. (1987) 84:161-165 O (Ly-5) cDNA reveals multiple transcripts Lymphocyte lineages. translated from GB/EMBL/DDBJ 29,'Y',331-336,'Y';'R',364-370,'X',372-375; }-649;669-680;725-731;'R',765-774;796-812; ,'X',939-942;960-971;1102,'X',1104-1108 :sum 2719 RES NID: g340850; PID: g548174 common antigens. US-08-951-733-20.rpr 0

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24-30,170-1291

*Status predicted *label MAT\
*domain extracellular *status predicted *label EXT\
product procein-tyrosine-phosphatase (T-cell varianc)
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*domain transmembrane *status predicted *label TMY\
*domain leukocyte common antigen cytosolic domain
homology *label LAC\
*domain intracellular *status predicted *label INT\
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SUMMARY

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587-1291 64.150,161,207,211, 218,253,258,290, 311,322,347,416, 427,457,489,520,

US-08-951-733-20.xpr

Page 26

Page 25 Page condent type 15:489 slabel KER

receidnes. The insertive form of the enzyme is composed of two regulatory chains and two catalytic enhances and a regulatory dimer that binds four catalytic enhances and a regulatory dimer that binds four cAMP molecules.

COMMENT Four types of regulatory chains are found: I-alpha, I-bets, II-alpha, and II-beta. Their expression waries among tissues and is in some cases constitutive and in others inducible.

Type II regulatory chains are phosphorylated by the activated catalytic chain. The physiological significance of catalytic chain by other kinases is unclear.

Type II regulatory chains modulate membrane association by binding to antichoring proceins, including the MAP2 kinase. The antichoring proceins, including the MAP2 kinase. The antichoring residues are essential for this binding and for CLASSIFICATION seminarfaction variances. ğ Mon Dec 21 09:28:27 1998 COMMENT ACCESSIONS
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#authors
#journal
#title ORGANISM DATE PEATURE 61-341 69-77 90 SUMMARY FEATURE 81-155 ecross-references MID-S0021306

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**sunnal Arch. Biochem. Biophys. (1991) 289:187-191

**sournal Arch. Biochem. Biophys. (1991) 289: RESULT ENTRY TITLE Db 291 LRPSLTGA 298 |||||||| Qy 372 LRPSLTGA 379 KEYWORDS egene CLASSIFICATION SSCROSS-references GB:M15474; NID:g337210; PID:g337211
GENETICS RESULT SUMMARY KEYWORDS CLASSIFICATION Dec 21 09:28:27 Overy Match 0.7%; Score 8; DB 1; Length 342; Best Local Similarity 100.0%; Pred. No. 1.64e-01; Matches 8; Conservative 0; Mismatches 0; Indels 0; Query Match 0.7%; Score 8; DB 2; Length 169; Best Local Similarity 100.0%; Pred. No. 1.64e-01; Indels Matches 8; Conservative 0; Mismatches 0; Indels across-references MUID:8100688 scross-references MU saccession S17058 52 EEEDTDPR 59 |||||||| 461 EEEDTDPR 468 couls_type protein idues 7 155-166 **label BRA The inactive form of the ensyme is composed of two regulatory Kerlawage, A.R.: Taylor, S.S.

J. Biol. Chem. (1980) 255:1483-0488

Govalent modification of an adenosine 3':5'-monophosphatebinding site of the regulatory subunit of chip-dependent
protein kinase II with 9-asidoadenosine
3':5'-monophosphate.
3':-monophosphate. _type protein
'B', 38-42 ##label POT A00518 517058
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Biochemistry (1984) 23:4200-4206
Mino acid sequence of the regulatory subunit of bovine type
Amino acid sequence of the regulatory subunit of bovine type
II admosine cyclic 3',5'-phosphate dependent protein
II admosine cyclic 3',5'-phosphate ONBOJE Stype complete
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15-ost-1982 sequence_revision 15-ost-1982 stext_change #domain protein kinase homology #label KIN\
#region protein kinase ATP-binding motif\
#active_site Lys #status predicted
#length 342 #molecular-weight 37970 #checksum 8888 esperfamily kinase-related transforming protein; protein kinase homology
Kinase homology
ATP; oncogene; phosphotransferase; serine/threonine-specific protein kinase; transforming protein superfamily cAMP-dependent protein kinase regulatory chain; cAMP receptor protein cyclic nucleotide-binding domain homology #domain caMP receptor protein cyclic nucleotide-binding domain bombology (fragment) #label CAP #length 169 #checksum 7365 noworky; duplication; heterotetramer; homodimer; phosphoprotein; phosphotransferase cAMP-dependent protein kinase II US-08-951-733-20 from porcine skeletal 0 Caps 0 0

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ACCESSIONS REFERENCE *authors *journal *title ##BOLGULE_UPP mRWA
#FREENCE A1477

FAVIor, S.S.
#authors Potter, R.L.: Taylor, S.S.
#journal J. Biol. Chem. (1979) 254:9000-9005
#journal Correlation of the cAMP binding domain with a site of
#title autophosphorylation on the regulatory submit of ORGANISM DATE RESULT ENTRY TITLE Db 8 LAPGFALLD 16 [[[]]]]]]]
Oy 119 LAPGFALLD 127 Hemmings, B.A.; Schwarz, M.; Adavani, S.R.; Jans, D.A.
stitle Expression cloning of a cDN encoding the type II regulatory
scross-references MUTI-1900/63
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scross-references MUTI-1900/63 Osery Match 0.8%; Score 9; DB 2; Length 1291; Best Local Similarity 100.0%; Pred. No. 1.20e-03; Osers Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps A35652 stype (raggents protein kinase (Cc 27.1.37), cAMP-dependent, type II-alpha regulatory chain - pig (fragments) common name domestic pig 0-Jun-1988 sequence_revision 05-Mar-1993 stext_change 25-Jan-1998 sequence_revision 05-Mar-1993 stext_change 25-Jan-1998 10-Jun-1998 10-Jun-

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egene CLASSIFICATION KEYWORDS

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ACCESSIONS REFERENCE *Authors *journal *title A26592
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A27 Virol. (1987) 61:889-887 at the mysloproliferative automated by a point mutation dat the mosonogene, has been modified as a selectable retroviral

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chains and two catalytic chains. Activation by cAMP produces two active catalytic monomers and a regulatory dimer that binds four cAMP molecules.

COMMENT

COMMENT COMMENT cays molecules.

Four types of regulatory chains are found: I alpha, I beta, II alpha, and II beta. Their expression varies among tissues and is in some cases constitutive and in others inducible.

The II regulatory chains are phosphorylated by the activated control to the control of the co

CLASSIFICATION (ssuperfamily cAMP-dependent protein kinase regulatory chain; cAMP receptor protein cyclic nucleotide-binding domain

PEATURE 1-134 135-256 KETWORDS nomology acetylated amino end; cAMP binding; duplication; heterotetramer; homodimer; phosphoprotein;

204,213 334,343 SUMMARY 48,211 -95 257-389 ddomain purtein interaction slabel DIPA

ddomain homp receptor protein cyclic nucleotide-binding

domain homology slabel CAIN

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domain homology slabel CAIN

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shinding_site phosphate (Thr) (covalent) (by

proline-directed kinase) status predictedN

shinding_site phosphate (Ser) (covalent) (by

autophosphorytation) status experimentalN

patholing_site cAMP (Clin, ANP) status predictedN

binding_site cAMP (Clin, ANP) status predictedN

Query Match 0.7%; Best Local Similarity 100.0%; Matches 8; Conservative Score 8; DB 1; Length 400; Pred. No. 1.64e-01; 0; Mismatches 0; Indels 0;

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Db 106 EEEDTDPR 113
Qy 461 EEEDTDPR 468

OKHUJR Stype complete
protein kinase (CC 27.1.137), cAMP-dependent, type II-alpha
regulatory thain - human
sformal_name from sapiens scommon_name man
1.mar-1993 secquence_revision 31-Mar-1993 stext_change
02-Sep-1997

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#length 404 #molecular-weight 45518 #checksum 9820

Query Match 0.7%; Best Local Similarity 100.0%; Matches 8; Conservative Score 8; DB 1; Length 404; Pred. No. 1.64e-01; 0; Mismatches 0; Indels 0; Gaps 0

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ACCESSIONS REFERENCE *authors *journal *title Nemura, O.; Rakahayashi, O.; Rishimori, K.; Misuno, S. Gene (1997) 165:217-222
The oDNA cloning and transient expression of a chicken gene encoding cytechrome P-450sec.
Adrenal gland
JC6200

eaccessio cession JC6200 **Smolecule_type mRNA **residuea 1-500 **label NOM **Cross-references DDD4:D49803; NID:g1906770; PID:d1019661; PID:g1906771

GENETICS

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CLASSIFICATION
RETWORDS
PEATURE
452 poscol
superfamily cytochrome P450
heme; steroid binding

SUMMARY *binding_site heme iron (Cys) (axial ligand) *status predicted *length 508 *smolecular-weight 58195 *checksum 7347

Query Match 0.7%; Score 8; DB 2; Langth 508; Best Local Similarity 100 0%; Pred. No. 1.64e-01; Matches 8; Conservative 0; Mismatches 0; Indels

128 PYGVLLKT 135 |||||||| 426 PYGVLLKT 433

ALTERNATE_NAMES 10 HRDYSI stype complete dnak-type molecular chaperone SSC1 precursor, mitochondrial yeast (Saccharomyees cerevisiae) endonuclease Scel JSK chain; endonuclease Scel large chain;

Page 31

heat shock protein 70-related protein SSCI; protein GTP654;

DRANISH formal_nume Sacchiromyces cerevisiae

JO-Un-1992 sequence_revision 30-Jun-1992 text_change

ACCESSIONS A3493; S11176; S20238; S1249; S57064; S63769

REFERENCE A3493; E.A.; Kramer, J.; Shilling, J.; Werner-Washburne, M.;

sauthors Bolmes, S.; Kosic-Smithers, J.; Micolet, C.M.

sjournal Mol. Cell. Biol. (1989) 9:3000-3008

stille SSCI, an essential member of the yeast HSP70 multigene

cross-reference MUID: 99384560

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REFERENCE #authors

Scherer, P.B.; Krieg, U.C.; Bwang, S.T.; Vestweber, D.; Schatz, G. BEGO J. (1990) 9-4315-4322 PREGO J. (1990) 9-4315-4322 A precursor protein partly translocated into yeast mitochondria is bound to a 70 kd mitochondrial, stress

*cross-references protein. ences MUID: 91092254 S12497

Page 29

ACCESSIONS REPERENCE *authors

etitle

US-08-951-733-20.rpr

Page 30

Mon Dec 21 09:28:27 1998

SO3885 SO3985 Oeyen, O.; Myklebust, F.; Scott, J.D.; Hansson, V.; Jahnsen,

PEBS Lett. (1989) 246:57-64

Ruman tests cDNA for the regulatory subunit RII-alpha of CAMP-dependent protein kinase encodes an alternate amino-terminal region.

ecross-references MIDIO Terminal region.

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**composed of two regulatory

chains and two catalytic chains. Activation by cAMP produces two

active catalytic monomers and a regulatory dimer that binds four

cAMP molecules.

**COMMENT Four types of regulatory chains are found: I-alpha, I-beta,

II-alpha, and II-beta. Their expression varies among tissues and

is in some cases constitutive and in others inducible.

Type II regulatory chains are phosphorylated by the activated

catalytic chain. The physiological significance of

to anchoring proteins, including the MAP2 kinase. The

amino-terminal 50 residues are essential for this binding and for

GENERICS

SEMETICS

Spence GDB:PREARCH

Sections: references GDB:120114; OMIN:176910

SECTION: Peter-Pp2

SEMETICATION SEMESTERMITY CAMP-dependent protein kinase regulatory chain; CLASSIFICATION CAMP receptor protein cyclic nucleotide-binding domain campain chair.

FEATURE 2-404 ovy ted amino end; cAMP binding; duplication; otetramer; homodimer; phosphoprotein;

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sproduct protein kinase, cAMP-dependent, type II-alpha etgalacory chain seatcus predicted slabel MNTN etgalacory chain seatcus predicted slabel MNTN etgalacory chain seatcus predicted slabel MNTN etgalacory chain control of the seatcus protein control of the seatcus protein control of the seatcus protein control of the seatcus predicted (ser) (seatcus predicted slabel camp, seatcus predicted, chinding_site cAMP (Glu, Arg) seatcus predicted chinding_site chinding

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Resultance Badcock, I submitted accession 548440
Findlequil-type DNA sendlequil-type DNA 1146
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H. STORMARSSION SUBSTITUTE TO the EMBL Data Library, June 1994
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##molecule_type DNA
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##resiones 1-234,'7',236-265,'TYCPRSGKN',274-479,494-652,658-1290,
##resiones 1.234,'7',236-265,'TYCPRSGKN',274-479,494-652,658-1290,
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escress-recerences GB:447047; EMBL:238062; NID:g603997; PID:g763351;
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Teast (1995) 11:61-78
Nucleotide sequence and analysis of the centromeric region of Yeast Chromosome IX.
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Goll (1992) 70:661-973
Translation initiation requires the PAB-dependent poly(A)
ribonuclease in yeast.
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uurr Genet. (1991) 19:495-502
Homology between mitochondrial DNA of Agaricus bisporus and
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itted to the EMBL Data Library, August 1994
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dyurnal Mol. Endocrinol. (1991) 5-938-648
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The Lowe's coulocorthorormal syndrome gene encodes a protein highly homologous to inositol polyphosphate-5-phosphatese-noise
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Blochem. Blophys. Res. Commun. (1991) 181:1131-1136
Blochem. Blophys. Res. Commun. (1991) 181:1131-1136
Identification and NB3-terminal amino acid sequence of three
insulin-like growth factor-binding proteins in porcine
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**Tresidues 1 - 1.11 **1.bbc.1 MAC

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senthires basey, H.; Keng, T.; Storma, R.K.; Vo.

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fdescription 7th sequence of 5. cerevisiae cosmid 9177.
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rice chioroplast
formal_name chloroplast Oryza sativa @common_name rice
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A81196 **Type fragment flyrestropin flyres
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Best Local Similarity 100.0%; Pred. No. 1.32+01;
Matches 7; Conservative 0; Hismatches 0; Indels
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#journal Proc. Natl. Acad. Sci. U.S.A. (1985) 82:7350-7363

#cross-references WID:85042665

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myosin catalytic light chain, ventricular and slow striated
muscle - nouse (fragment)
myosin alkali light chain
sformal_name hiss musculus scommon_name house mouse
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hypothetical protein YRM212c - yeast (Saccharomyces
hypothetical protein YRM260c
sformal_name Saccharomyces cerevisiae
02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change
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Ly-5-8 glycopyretein - mouse (fragment)
#formal_name Mus musculus #common_name house mouse
05-Jun-1987 *sequence_revision 05-Jun-1987 *text_change
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       $77068 stype complete
hypothetical protein - Synechocystis sp. (PCC 6803)
sformal_name Synechocystis sp.
pcc 6803
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S.; Buckingham, M.E.
Nucleic Acids Res. (1989) 16:10037-10052
Promoter analysis of myosin alkali 19th chain genes
expressed in mouse striated muscle.
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Pred. No. 1.32e+01;
0; Mismatches 0; Indels
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This sequence was derived from a human cytotoxic T-lymphocyte that is T3+,T4+, T8-.

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811 AVVIEQS 817
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**residues 1-139 **label LEI
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T-cell receptor alpha chain precursor V region (CTL-L17)
humal name Homo sapiens scommon_name man
17-Mar-1987 sequence_revision 17-Mar-1987 stext_change
02-Sep-1997
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Immunogenetics (1986) 24:17-23
The complete primary structure of the T-cell receptor genes
from an allowactive cytotoxic human T-lymphocyte clone.
ces. MJID:86378770
rakihara, Y.; Reimann, J.; Michalopoulos, E.; Ciccone, E.;
Moretta, L.; Mak, T.W.
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Bakamuta, Y. Hiyajima, N.; Hitosawa, M.; Sujitra, M.;
Samamoto, S.; Kimura, T.; Hosunchi, T.; Matsuno, A.;
Kuraki, A.; Makasaki, N.; Batuo, K.; Okumura, S.; Shimpo,
S.; Takeuchi, C.; Mada, T.; Watanaba, A.; Kamada, M.;
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Pred. No. 1.32e+01;
0; Mismatches 0; Indels 0; Gaps
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Pred. No. 1.32e+01;
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SUMMARY
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27-168
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Qy 697 LLGASVL 703
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Qy 697 LLGASVL 703
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Best Local Similarity 100.0%;
Matches 7; Conservative
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#molecut_type DMA
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#cross-references GB:85692; MID:9298654; PID:9298655
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121-125
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*accession UC5478
*arablecule_type_DDM,
*arableus_type_DDM_DB3118, HIS
*arableus_type_DDM_DB3118, HID:g1183837; PID:d1012484; PID:g1183840
**sexperimental_pource_strain_PAO1
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205476
Hishida (T. Ivasaki, H.; Ishioka, K.; Shinagawa, H.
Gene (1995) 192163-70
Rolecular analysis of the Pseudomonas acruginosa genes, ruvk,
ruvB and rucc, involved in processing of homologous
recombination intermediates.

    Exp. Med. (1999) 159:393-405
    Diversity and exturcture of human T call receptor delta chain
genes in peripheral blood gamma/delta-bearing T

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Roper, D.I.; Gentt (1993) 237:241-250
The Escherichia coli C homprotocatechnate degradative operon: he gene order, direction of transcription and control of expression.
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glycoprotein; heterotetramer; receptor; T-cell
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DNA binding; transcription regulation
#length 148 #molecular-weight 17355 #checksum 5904
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predicted
#length 139 #molecular-weight 15441 #checksum
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Pred. No. 1.32e+01;
0; Mismatches 0; Indels 0; Gaps
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SUMMARY

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Ocery Acach 0.6%; Score 7, DB 2; Length 174; Best Locatch Similarity 100.0%; Pred. No. 1.32e+01; Macches 7; Conservative 0; Mikmanches 0; Indels 0; Gaps

*product endodeoxyribonuclease ruvc *status predicted *label BAT *length 174 *molecular-weight 18556 *checksum 8754

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Best Local Similarity 100.0%; Pred No. 1,32+01; Indels 0; Gaps
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps
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242 GARREGG 248
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856 GSILSTL 862
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yop20 protein reration entercoolitica
#formal_name Yersinia entercoolitica
#formal_name Yersinia entercoolitica
25-pab-1994 sequence_revision 10-Rov-1995 *text_change
09-sp-1997
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Michiels, T.; Wattiau, P.; Brasseur, R.; Ruysschaert, J.M.;
Correliu, G.
Correliu, G.
Infect, Immun. (1990) 58:2840-2849
@erretion of rop proteins by Yersiniae.
1814-1011-90354044
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myosin alkali light chain 3, ventricular and slow skeletal
musele - rat
musele - rat
MCLab; MCL'N; myosin Li catalyric light chain, cardiac
musele; ventricular myosin light chain 1
formal_name Rattus norvegicus fcommon_name Norway rat
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#length 182 #molecular-weight 20828 #checksum 1492
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Best Local Similarity 100.0%; Pred. No. 132+01;
Matches 7; Conservative 0; Minmatches 0; Indels 0;
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                                                                  31
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*formal_name Mycoplasma pneumoniae
Arcc 2943
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569588 stype complete hypothetical protein YDR533c - yeast (Saccharomyces
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hypothetical protein ydhK - Bacillus subtilis
eformal_name Bacillus subtilis
05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
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superfamily calmodulin; calmoding peach homology
blocked maino end; calcium binding; cardiac muscle;
duplication; EF hand; muscle contraction; skeletal muscle
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#modified_site blocked amino end (Pro) (in mature form)
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O; Mismatches O; Indels O;
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#formal_name Saccharomyces cerevisiae
22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change
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Submission submitted to the DMB: Data Library, August 1995

edescription The acquence of S. cerevisiae commids 9166, 9787, 9717, and

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**Bauthor**

Dijkema, R., Dekker, B.M.M.; van Ormondt, H.; de Waard, A.;

**Pournal Gene (1980) 13.287-299

**Licia Gene organization of the transforming region of weakly

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***Erross-references GB:D49488
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Babyen, J. (1998-141; Inoue, K.
Babyen, J. (1998-141-141; Protein: GDN cloning,
Hamber alpha tocopherol Grasse protein: GDN cloning,
Hamber and chromosomal localization.
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alpha-tocopierol transfer protein - human
fformal_name Homo sapiens fcommon_name man
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*cross-reference NUID:97061301

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**status 970610

**statu SUMMARY O.84; Score 7; DB 1; Length 261;
Best Local Similarity 100.0%; Pred. No. 1,12s+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps Query Match 0.6%; Score 7; DB 2; Length 262; Best Local Similarity 100.0%; Pred. No. 1.32e+01; 178 LLCSLCY 184 ||||||| 862 LLCSLCY 868 1 sproduct early EIA 24K protein sstatus predicted slabel
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e1ength 261 smolecular-weight 28385 schecksum 884 Yaudd, M.: Tabeta, S.

DNA Res. (1986) 3:109-118
Sequence analysis of the genome of the unicellular
cyanobacterium Symenboystis sp. PCC6803. II. Sequence
determination of the entire genome and assignment of
potential protein-coding regions.

nees MVID:97061201 predicted
slength 262 *molecular-weight 29926 *checksum 8162 576610 ftype complete hypothetical protein - Symechocystis sp. (PCC 6803) formal_name Symechocystis sp. PCC 6803 25-Apr-1997 sequence_revision 25-Apr-1997 stext_change 05-Dec-1997 noko, T. Sato, S., Rotani, H., Tanaka, A., Asamisu, E., Rakamura, Y. Hiyejiam, N., Hitosawa, M.; Sugitra, M.; Baamato, S., Kiaura, T.; Hoseuchi, T.; Hatsuno, A.; Huraki, A.; Hatsaki, M.; Matuo, K.; Okimura, S.; Shimpo, S., Taksuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; 0

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submitted to the EMBL Data Library, February 1995
GO1727 Ouahchi, K.; Arita, M.; Kayden, H.; Hentati, F.; Hamida, M.B.; Sokol, R.; Arai, H.; Inoue, K.; Mandel, J.L.; Koenig, M.

Nature Genet. (1995) 9:141-145
Ataxia with isolated vitamin E deficiency is caused by mutations in the alpha-tocopherol transfer protein.
\$52466

B5937 stype complete
conserved hypothetical protein AF7298 - Archaeoglobus
fulgidus
fiormal_name_Archaeoglobus fulgidus
05-Dec-1997 seequence_revision 05-Dec-1997 stext_change
05-Dec-1997

Klebk H.P.; Clayton, R.A.; Tomb, J.P.; White, O.; Melson, K.Z.; Ketchum, K.A.; Dodson, R.J.; Gvinn, M.; Hickey, E.K.; Petcason, J.D.; Michardson, D.L.; Kerlawage, A.R.; Gyraham, D.E.; Kyryledes, M.C.; Pielschmann, R.D.; Quckenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.P.; Dougherty, B.A.; McKenny, K.; Adams, M.D.; Loftus, B.; Petcarson, S.; Reich, C.I.; McHell, L.K.; Badger, J.H.; Glocky, G. B.; McChan, J.D.; Weldman, J.D.; Weldman, J.P.; Weldman, J.P.; Weldman, J.P.; Weldman, B.P.; Syrkes, S.M.; Sadow, P.W.; Domann, C.; Donybers, C.H.; Sadow, P.W.; McTesh, K.P.; Domann, C. J.; Fraez, C.H.; Sathit, H.O.; Mocese, Mason, T.M.; Olsen, G.J.; Fraez, C.H.; Sathit, H.O.; Mocese,

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**status Preliminary; nucleic acid sequence not shown;

**consecute type mRNA.

**residues 1-316 **slabel DEC

**cross-references EMBL:X56537

**snote the nucleotide sequence was submitted to the EMBL Data

**cross-references EMBL:X56537

**snote the nucleotide sequence was submitted to the EMBL Data

**CLASSIFICATION **superfunity unsassigned homeobox proteins; homeobox homology

**EXTURES DNA binding: homeobox: nucleus; transcription regulation

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Devies, S.S.P.; Krishnapillai, V.V.
submitted to the EMBL Data Library, September 1990
DBM sequence analysis of the replication region of the
Pseudomonas acruginosa plasmid 891-5.
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EMBO J. (1993) 12:4053-4062
Molecular genetic analysis of a locus required for resistance
to antimicrobial peptides in Salmonella typhinurium.
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Wittle The complete genome sequence of Escherichia coli K-12.

**Recommendation** Heavier Science Mullipsychology

**Recommendation** He
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A64720, F.R.; Plunkett III, G.; Bloch, C.A.; Perma, N.T.;
Burland, V.; R.lay, M.; Collado-Vides, J.; Glasner, J.D.;
Ecde, C.K.; Myhev, G.F.; Gregor, J.; Davis, M.W.;
Katheptrick, M.A.; Coeden, M.A.; Bose, D.J.; Mas, B.; Shao,
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dnaw_protein synechocystis ap. (PCC 6803)
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E59219 ftype complete conserved hypothetical protein MTH894 - Methanobacterium thermoautorrophicum (strain Delta H)
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peptide transport system permease protein SapB - Escherichia
coli (strain K.12)
fformal.name Escherichia coli
12-Sep-1997 ftext_change
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homeotic protein - human
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ANUTHORS Soloaki, M.J.: Uhr. J.W.: Vitetta, E.S.
FOURDAL MATURE (1982) 266,759-761
Fittle Pinary structural studies of the Qa-2 alloantigen:
Fittle implications for the evolution of the MMC.

ACCORDANCE MULD:8217202

***cross-references MULD:8217202

***cross-references MULD:8217202
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Best Local Similarity 100.0%; Pred. No. 1.32e-0;
Matches 7: Conservative 0; Mismatches 0; Indels 0;
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Mancok, G.L.: Sherman, D.H.; Calvin, S.; Allen, H.; Flavell, R.A.

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J. Exp. Med. (1987) 165,1359-1370

Tissue-specific expression of cell-surface Qa-2 antigen from the complex of the co
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superfamily class I histocompatibility antigen:
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submitted to the EMBL Data Library, July 1995
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omplete genome sequence of Methanobacterium
thermoautotrophicum Delta H: functional analysis and
comparative genomics.
us MID:98037514
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'XX',46,'L',48-49,'XXXX',54,'X',56-57 eglabel SOL
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is, J.; Aldredge, T.; Bashirradch, R.; Blakety, D.;
R.; Gilbert, K.; Harrison, D.; Heang, L.; Kesgle, P.;
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Bush, D.; Safer, R.; Paterell, D.; Pabhakar, S.;
ugali, S.; Shimer, G.; Goyal, A.; PietroRovski, S.;
Og, L.; Danielas, C.J.; Mao, J.; Rice, P.; Roselling,
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Relabors Folia, K.A.; Bunt III, S.W.; Bunkspiller, T.; Sun, Y.H.;
Flournal J. Exposed (1989) 170.1837-1856
Fittle Comparison of exon 5 sequences from 35 class I genes of the
Fittle Ship/c mouse.

Frescher Bhib/c mouse.

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formal_mame Homo sapiens fcommon_name man

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acetoin dehydrogenase El component (TPP-dependent beta
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formal_name Bacillus subtilis
65-pec-1997 #sequence_revision 05-pec-1997 #text_change
05-pec-1997 Redar, V.; Fletcher, L.; Powell, L. Biochem, Biophys. Res. Commun. (1996) 226:461-465 Biochem, Biophys. Res. Commun. (1996) 236:461-465 Biochem, Biochys Res. Commun. (1996) 226:461-465 Molecular cloning of a novel manh shiphly expressed in haemochromatotic human liver and proliferating cells. and . Caps o,

PC4211 stype fragment hepatocellular carcinoma complicating haemochromatotis protein - human (fragment)

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Schroeter, R.; Soctfone, P.; Sektyuchi, J.;
Serror, S.J.; Serror, P.; Shin, B.S.; Soldo,
Serror, S.J.; Serror, P.; Shin, B.S.; Soldo,
Takeuchi, M.; Takegi, T.; Takahashi, H.;
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Fournal Gene (1994) 144;143-144.
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Score 7; DB 2; Length 347; Best Local Similarity 100.0%; Pred. No. 1.32+01; Matches 7; Conservative 0; Mismatches 0; Indels 0;
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molicule_type DNA
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RIMA POLYMENAER BETA SU
A GLIVANATE STRITHASE (M.
CENOME POLYPROTEIN (CO
CAD PROTEIN (CONTAINS)
GENOME POLYPROTEIN (CO
CENOME POLYPROTEIN
MICROTUBULE-ASSOCIATE
MONSTRUCTURAL POLYPROT
PECANEX POTEIN
A PICTOTUBULE-ASSOCIATE
ANDENOMATOUS POLYPROT
PECANEX POLYPROTEIN (CO
ADDITIONAL SIMPROTEIN (CO
CENOME POLYPROTEIN (CO
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TISSUET-TCELL;
TISSUET-TCELL;
MEDLINE, 8604365.
MEDLINE, 804365.
MEDLINE, 80436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [2]
REVISIONS.
SAGA Y., TUNG J.-S., SHEN F.-W., BOYSE E.A.;
PACC. NATL. ACAD. SCI. U.S.A. 84:1991-1991(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1998
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J. -S.,

CANTOR

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RESULT 1

ID CHALPOUSE STANDARD; PRT; 1152 AA.
AC PO6800;
DT 01.43M-1988 (REL. 05, CREATED)
DT 01.43M-1988 (REL. 05, CREATED)
DT 01.43M-1988 (REL. 05, LAST SEQUENCE UPPARE)
DT 10.70M-1987 (REL. 35, LAST ANNOYATION UPPARE)
DE ISOPOSIT COMMON ANTIGEN LT-5 PRECURSON (RC 3.1.3.48) (30
CH PIPRC, CHAPTOCAS, CHORDATA; VERTEBRATA; TETRAPODA; HAMMA
RN 111 ANNOYATION REPROM N. A.
RN SHOLNE; RODENTIA.
RN SEQUENCE FROM N. A.
RN LILING; RS131866.
RN PROC. NUTL. ACAD. SCI. U.S.A. 83.6940-6944(1986).
                                         STATE STATE OF STATE 
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ACT_SITE
CARBORYD
CARBO
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                                PROTEIN-TYROSINE PROSPHATASE.
BY SIMILARITY.
BY SIMILARITY.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-951-733-20.rsp
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RA BASCHEE W.C.;

RI AND SCHEEN C. 1. S. A. 84.161-165(1987)

RI PROC. NAT. ACAD. SCI. U.S.A. 84.161-165(1987)

RI PROC. TO STATE ACAD. SCI. U.S.A. 84.161-165(1987)

RI PROC. NAT. ACAD. SCI. U.S.A. 84.161-165(1987)

RI PROC. NAT. ACAD. SCI. U.S.A. 84.161-165(1987)

RI PROC. NAT. SCI. U.S.A. 84.161-165(1987)

RE PROC. SCI. U.S.A. 84.161-165(1987)

RE PROC. NAT. SCI. U.S.A.
              SEQUENCE OF 822-1152 FROM N.A.
MEDILINE; 87092355.
RASCHEE W.C.;
PROC. NATL. ACAD. SCI. U.S.A.
-1- FUNCTION: REQUIRED FOR T-C.
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ALIGNMENTS

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RESULTS J

DE STANDARD: PRT: 305 AA.
AC 0273-1989 (REL. 10. CREATED)
DT 0.1-MAR-1989 (REL. 10. CREATED)
DT 0.1-MAR-1989 (REL. 10. LAST RECURENCE UPDATE)
DT 15-UT-1999 (REL. 13. LAST MANOVATION UPDATE)
DE UDALIL-DHA GLYCOSTLASE (EC 3.2.2.) (UDG).
OS VARICELLA-COSTEN VIRUS (STRAIN DUMAS) (VEV).
OC VIRIDE: 19-NOA REWELOPED VIRUSES; HERPESVIRIDAE; ALP
RN 111
RP SEQUENCE PROWN A.M.
RX MEDILIRE: 68306657.
RA DAVISOR A.J. SCOTT J.E.;
RL J. GEN. VIROL. 67:1159-1816(1986).
TH. GARTOLTON EXCELSES UNCLIL RESIDUES FROM THE DNA WH
GC 1- PUNTREMAS ON DET 90 DEMINATION OF DUME RESIDUES
CC 1- SULTMERAS ON DET 90 DEMINATION OF CUTOSINE.
DE SEQUENCE DE SULTMERAS TO THE UNACLI-DHA GLYCOSTLASE
DE STR. LG72115 DENSES 9
DTR. LG72115 DENSE 9
DTR. LG72115 DENSES 9
DTR. LG72115 DENSE 9
D
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CC ANONG TISSUES AND 15 IN SOME CASES CONSTITUTIVE AND IN OTHERS
CC -1- PM: PROSPHORYLATED BY THE ACTIVATED CATALITIC CHAIN.

PM: PROSPHORYLATED BY THE ACTIVATED CATALITIC CHAIN.

PM: ASSES: ASSES: ASSES:
DR PHR: ASSES: 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.7%;
Best Local Similarity 100.0%;
Matches 8; Conservative
(1)
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE: 68:06657.

J. GEN. VIRGL. 67:1759-1816(1986).

J. GEN. VIRGL. 67:1759-1816(1986).

J. GEN. VIRGL. 67:1759-1816(1986).

J. GEN. VIRGL. 86:1759-1816(1986).

PROCEPTELSE EXCUSSES MICHIEL RESIDUES FROM THE DIA WHICH CAN ARISE
AS A RESULT OF MISTINCOEPORATION OF DUMP RESIDUES BY DIA
DIXTERISE OR DUE TO EDMINIATION OF CITCOSTIA.SE FAMILY.

DEBL. MOLITO, 66:0048 - .

DIX. GA77115, DOBESSO.

PROSITE: P800130; U_DNA_GLYCOSTIA.SE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 EEEDTDPR 59
|||||||||
461 EEEDTDPR 468
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2 >155 CAMP.
50 150 CAMP.
155 155 CAMP.
170; Score 8; DB 1; Le
0 ord: No. 4.71e-07
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Pred. No. 4.71e-02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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(FRAGMENT).
PRENAZA:
SUS SCROPA (PIG).
EUKARYOTA; METAZOA; CHORDATA;
EUTHERIA; ARTIODACTYLA.

TETRAPODA;

CHAIN

SECURNE: 87007 N.A.

HERMINGS B.A., SCHWAR H., ADAVANI S.R., JANS D.A.;

HERMINGS B.A., SCHWARZ H., ADAVANI S.R., JANS D.A.;

HERMINGS B.A., SCHWARZ H., ADAVANI S.R., JANS D.A.;

PERS LETT. 709:119-2121(1986).

1 PURCTION: TIPE IN PEGULATORY CHAIRS, INCLIDING THE MAPP KINSE.

1 SUBUNIT: THE INACTIVE FORM OF THE ENTINE IS COMPOSED OF TWO

1 SUBUNIT: THE INACTIVE FORM OF THE ENTINE IS COMPOSED OF TWO

1 SUBULATORS CHAIRS AND TWO CATALITIC CHAIRS. ACTIVATION BY CAMP

PRODUCES TWO ACTIVE CATALITIC MONOMERS AND A REGULATORY DIMER

THAT BILDS FOUR CAMP MOLECULES.

TAP2_PIG STANDARD; PRT; 155 AA. . P0520; 10: AGC-1987 (REL. 05, CREATED) 11-AGC-1987 (REL. 05, LAST SEQUENCE UPDATE) 11-AGC-1987 (REL. 05, LAST SEQUENCE UPDATE) 11-AGE-1986 (REL. 05, LAST ANNOTATION UPDATE) CAMP-DEPENDENT PROTEIN KINASE TYPE II-ALPEA RESULATORY

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8 LAPGFALLD 16 |||||||| 119 LAPGFALLD 127

Query Match 0.8%; Best Local Similarity 100.0%; Matches 9; Conservative

Score 9; DB 1; Length 1152; Pred. No. 2.00e-04; 0; Mismatches 0; Indels

ő

Gaps

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DNA REPAIR; HYDROLASE; GLYCOSIDASE.
ACT_SITE 148 148 GENERAL BASE (BY SINILARITY).
SEQUENCE 305 AA; 34376 MM; ODD3B64F CRC32;
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US-08-951-733-20.xsp

Ouery Match 0.7%; Score 8: DB 1: Length 305; Best Local Similarity 100.0%; Pred No. 4.72e-02; Matches 8: Conservative 0: Mismatches 0; Indels 0;

Caps

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REGULER OF 1-55 FROM N.A.

REGULER JULISES

A POSSES

REGULER JULISES

REG
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**HIEL J. STOCKING C., STACEY A., OSTERTAG W.;

**J. VIROL. SI-889-197(1987).

- VIROL. SI-889-197(1987).

- INTERVALUE WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-CE-PROTEIN KINASES.

- PROTEIN KINASES.

- PROSITE: PROGULO; PROTEIN KINASE_ATP: 1.

- VINASEPRASES, ESENIEC/THERRINGE.

- VINASEPRASES.

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Best Local Similarity 100.0%; Pred. No. 4.71e-02;
Matches 8; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%;
Matches 8; Conservative
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BINDING 343
SEQUENCE 400 AA;
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[||||||
105 RVLQRLCE 112
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P1161: 016821; 13 CREATED)
01-JAN-1990 (REL. 13 LAST SEQUENCE UPDATE)
01-JAN-1990 (REL. 13 LAST ANNOCATION UPDATE)
01-JAN-1990 (REL. 36, LAST ANNOCATION UPDATE)
CAMP-DEPENDER; PROFIES N. KINSE TYPE II-ALPHA REGULATORY CHAIN.
PRANAIA ON PRKAJ OR PRANEZ.
BONG SAPIENS (RUMAN)
BONG SAPIENS (RUMAN)
LONG SAPIENS (RUMAN)
LONG SAPIENS (RUMAN)
LONG SAPIENS (RUMAN)
LONG SAPIENS (RUMAN)
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461 EEEDTDPR 468
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P10431;
01-MR-1399 (REL. 10, CREATED)
01-MR-1399 (REL. 10, LAST EQUINACE UPDATE)
01-MR-1399 (REL. 13, LAST ANNOTATION UPDATE)
01-MR-1399 (REL. 13, LAST ANNOTATION UPDATE)
101-MR-1399 (REL. 14, LAST ANNOTATION UPDATE)
101-MR-1399 (REL. 15, LAST ANNOTATION UPDATE)
101-MR-1399 (REL. 16, LAST ANNOTATION UPDATE)
101-MR-1399 (REL. 10, LAST ANNOTATION UPDATE)
101-MR-1399 (REL. 31, LAST ANNOTATION UPDATE)
1
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TISSUE-TESTIS:
REDILNE: 89211413.
OYEN O., MYNLDBUST P., SCOTT J.D., HANSSON V.,
PEBS LETT. 246:37-64(1989).
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         291 LRPSLTGA 298
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372 LRPSLTGA 379
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RIDAE: SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE:
COVIRIMAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63
69
90
198
342 AA;
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77
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198
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37970 MW;
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343 C
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
MW; 1C56243C CRC32;
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Pred. No. 4.71e-02;
0; Mismatches 0;
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CAMP.
: 197A0D99 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-951-733-20.rep
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JAHNSEN
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DE CALE-POULLY

POSILS

OF 21-UD-1986 (REL. 01. CREATED)

DT 21-
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C. -1- PYK: A SECOND PROSPHORILATION SITE HAS NOT BEEN LOCATED.

MR PIR: A OSCIAL SECOND PROSPHORILATION SITE HAS NOT BEEN LOCATED.

MR PIR: S17058: S17058.

MR PROSITE: PROSPHORIZATION: MULTICENE FAMILY;

MR PROSITE: PROSPHORIZATION: MULTICENE FAMILY;

MR ACRETICATION: DISSURPLING.J: 2.

MR PROSITE: PROSPHORIZATION: MULTICENE FAMILY;

MR ACRETICATION: JO-STRUCTURE.

MR ACRETICATION: DISSURPLING J: CAMP.

MR ACRETICATION: JO-STRUCTURE.

MR AC
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Best Local Similarity 100.0%;
Matches 8; Conservative
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BLOCHMISTRY C.S. 143.154(1987).

- SUBGUILT. THE INACTIVE POWN OF THE ENERGY S. ACTIVATION BY CAMP
PRODUCES TWO ACTIVE CANALTIC CHAIRS AND A REGULATORY DIMERS
THAT BIMES FORM CAMP DECEDIAGES AND A REGULATORY DIMERS
THAT BIMES FORM CAMP DECEDIAGES OF REGULATORY CHAIRS ARE POWNS
- TISSUES SPECIFICITY. FOUR TYPES OF REGULATORY CHAIRS ARE POWNS
- TISSUES SEEN, IT. ALPHAN, AND ITSEEN, HILLIE EXPENSESSON VARIES
ANDORTHLES
- NERONITATIONS AND IS IN SOME CASES CONSTITUTIVE AND IN OTHERS
- INDOCTING.
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BOS TARROS (BOVINE),
BUILANCOTA, METAGOA, CHORDATA; VERTEBRATA; TETRAPODA; HAMMALIA;
ETTHERIA; ARTIODACTITA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HE97, IRAST STANDARD: PRT; 654 AA.

P1138;
01-0CT-1996 (REL. 12, CREATED)
01-0CT-1996 (REL. 12, LASTATED)
01-0CT-1996 (REL. 14, LASTANDARION OFDATE)
01-0CT-1996 (REL. 14, LASTANDARION OFDATE)
MITOCHOMBRIAL HEAT SHOCK PROFERM SCRIP PRECURSOR (ENDONUCLEASE MID SEMBURIT). REAL SHOCK OR J1639.

SECTIANDAMICES CEREVISIANE (BARER'S TRAST).
DIMARUTA: FUNDAL ACCONTOCITAL HEALACCONTCETES.
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461 EEEDTDPR 468
                                                                                                                                                                                         SENOURNE FROM N.A.
SENOURNE FROM N.A.
SENOURNE 89384560.
CRAJE E.A. KRAMER J., SHILLING J., WERNER-WASHEURNE M.,
KOSIC-SHITHERS J. NICOLET C.M.
MOSIC-SHITHERS J. S. DOCO-2006(1989).
MOL. CELL BIOL. 9.3000-3006(1989).
                          SEQUENCE FROM N.A., AND SEQUENCE OF 24-41.
STRAIN-IAM 4274;
MEDLINE: 90368701.
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889; CNMP_BINDING_2; 2.
042; CNMP_BINDING_3; 2.
PHOSPHORYLATION; DUPLICATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      346
45387 MN;
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PROSPHORTIATION (BY SIMILARITY).
CAMP.
CAM
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Pred. No. 4.71e-02;
0; Mismatches 0; Indels
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ENTYME

Page 28

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Gaps 6

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MORISHIMA N., NAKAGAWA K., YAMAMOTO E., SHIBATA T.; J. BIOL. CHEM. 265:15189-15197(1990).

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Page 29
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STANDARD;

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Page 30

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RESOLT PERSOLT RESOLT PERSOLT PERSOL
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RE SEMENTIPE MAY-1995) TO BRE/GENERAIR/DEBJ DATA BANGS.

RI SUBSTITUE MAY ASS INVOIRES IN INOSTOL BOSCHATE BETANOLISM.

RI FUNCTION MAY BE INVOIRES IN INOSTOL BOSCHATE BETANOLISM.

C. -- TESSUS SERVICITT: BHAIN, SEGLETAL MOSCLE, BEART, KIDNET,

C. -- LINSUS BETANDER BANGS BANGS OF LOSS'S COULDERBRORENAL

SYNDROME DEFENSIONAL MATERIAL BY HIPROPHYMALATIA, CATAMACT,

SYNDROME DEFENSIONAL RESULTION BE STANT RICKETS, ANIMOACIDERAL

SYNDROME DAMAGNAME PRODECTION BE STANT RICKETS, MATROACIDERAL

AND REAL PROSPRIATAS TO THE INOSITOL-1,4,5-TRISPHOSPHATE

SPROSPHATAS TOPE IN PARTICLE

SPROSPHATAS STATE IN PARTICLE

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BRILL STATE 218935 ...

MATERIAL PROSPHATAS STATE STATE BANGS BANG
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SPACE.

SPACE.

C: SPECELLAR LOCATION: MITCHONDRIAL MATRIX. DETECTED ALSO IN THE C: SUCCELLAR LOCATION: MITCHONDRIAL MATRIX. DETECTED ALSO IN THE C: SIMILARITY STRONGES TO THE HEAT SHOCK PROPERN 70 FMMIX. STRONGEST C: SIMILARITY STRONGES TO THE HEAT SHOCK PROPERN 70 FMMIX. STRONGEST C: SIMILARITY STRONGES TO THE HEAT SHOCK PROPERN MITCHONDRIAL HESPTO AND WITH BACTERIAL DNAK. BENEL, MS5375, G171463; ...

REMEL, 
                                                             SRUT 10

PRINI YAST STANDARD; PRT; 1480 AA.

PRISCIPLE STANDARD; PRT; 1480 AA.

PRISCIPLE STANDARD; PRT; 1480 AA.

PRINI PROTEINS (REL. 27, CREATED)

1 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)

1 01-ROW-1997 (REL. 33, LAST ANNOTATION UPDATE)

2 PANI PROTEINS CREEVISTAE (BAER'S YEAST).

5 SACCHARONICS CREEVISTAE (BAER'S YEAST).

5 SACCHARONICS CREEVISTAE (BAER'S YEAST).

5 CHARTOTA: FUNGI: ASCONTCOTINA: HEMIASCONYCETES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.7%;
Best Local Similarity 100.0%;
Matches 8; Conservative
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Best Local Similarity 100.0%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   30 LPAPGARR 37
||||||||
238 LPAPGARR 245
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MEDIHE, 9.09254.

MEDIHE, 9.09254.

SCHERER P.E., RRIEG G.C., HWANG S.T., VESTWEEER D., SCHATZ G.;

SCHERER P.E., SKRIEG G.C., HWANG S.T., VESTWEEER D., SCHATZ G.;

EGGO J. 9:4315-4322(1990).

10: PHOTION: SCCI IS AN ESSENTIAL HITOCHONDRIAL PROTEIN, IT

11: PHOTION: SCCI IS AN ENTOCHONDRIAL HIT ANY INITIATE HER EVENTS

COMPLEXES INSIDE THE HITOCHONDRIAL IT ANY INITIATE HER EVENTS

THAT LEAD TO REPOLDING OF IMPORTED PRECUNSORS IN THE MATRIX

THAT LEAD TO REPOLDING OF IMPORTED PRECUNSORS IN THE MATRIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGD; L0000561; S; PROSITE; PS00297 PROSITE; PS00329 PROSITE; PS00329 PROSITE; PS01036 HEAT SHOCK; ATP-ITRANSIT PEPTIDE. TRANSIT PEPTIDE.
SEQUENCE FROM N.A., AND SEQUENCE OF 320-344; 352-375 AND 899-906. MEDLINE; 92405166.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTDROLASE.
CONFLICT 660 660 G -> E (IN REF. 2).
SEQUENCE 968 AA; 111485 MW; 53CE3BE2 CRC32;
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EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 09:28:29 1998
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15SSTE-RICHER
HEDLINE: 9334430.
HEDLINE: 9334430.
H., OKABE I., BAILEY L.C., NELGON D.L.,
LEWIS R.A., MCINES R.R., NUSSBAUM R.L.;
LEWIS R.A. MCINES R. R. WISSBAUM R.L.;
NUTRE 358:239-242(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     595 LKELVARV 602
||||||||
99 LKELVARV 106
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STRAIN=S388C;
WEDLINE; 95397595.
WEDLINE; 95397595.
WEAST 11:775-781(1995).
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| P200291, HS970_1, 1.
| P2001291, HS970_3, 1.
| P201046, HS970_3, 1.
| P201046, HS970_3, 1.
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654 AA;
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70627 MH;
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ASN-RICH.
ASN-RICH.
N -> NN (IN REF. 2).
G -> D (IN REF. 2).
44; 0EB32F62 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 8; DB 1; Length 968; Pred. No. 4.71e-02; 0; Mismatches 0; Indels
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Pred. No. 4.71e-02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TETRAPODA; MAMMALIA;
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AC P30322;
DT 01.4pr.1993
DT 01.4pr.19
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DT 01
OC QC
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Best Local Similarity 100.0%;
Matches 8; Conservative
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|||||||
969 SSYARTSI 976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 09:28:29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SACHS A.B., DEARDORFF J.A.;
CELL 70:961-973(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        797 AA.
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RP SEQUENCE PROM N.A.

RP SEQUENCE PROM N.A.

RP SEQUENCE PROM N.A.

RE YEARLANGE SEC.

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C. --- CAUTION NOT KNOWN.

C. --- CAUTION NOT KNO
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CON EPERANTOPIA, FUNGI; BASIDIONYCOTINA.

RN (1)

RN (1)

RN (2)

RN (2)

RC STRAIN-ARC 24666 / Ac4;

RX MEDIZINE; 9.137410.

RA MEDIZINE; 9.137410.

RA MEDIZINE; 9.137410.

RA MEDIZINE; 9.137410.

RA MEDIZINE; 19:495-502(1991).

CC -1 CHALLATTE (ATTIVITE: N EDEXINGLEOSIDE TRIPHOSPHATE =

RY PYROPHOSPHATE + DNA(H).

CC -1 THIS DNA POLYMERASE REQUITIES A PROTEIN AS A PRIMER

CC -1 THIS DNA POLYMERASE REQUITIES A PROTEIN AS A PRIMER

CC -1 SKILLARITE; BEDONGS TO DNA POLYMERASE TYPE-5 PAMIT. STRONG TO COMPANIANTE STRONG TO COMPAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCEL_HUMAN STANDARD: PRT: 968 AA.

Q01965; Q15640; E. 25, CREATED)

Q1-7U1-1993 (REL. 25, CREATED)

Q1-7U1-1994 (REL. 25, LAST SEQUENCE UPDATE)

15-7U1-1996 (REL. 25, LAST ANDORATION UPDATE)

LORE'S CULLOCEREBRORENAL SYNDROME PROTEIN.

GORD. SAPIENS (HUMAN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SENDENCE PROM N.A.
SENDENCE PROM N.A.
SENDENCE PROM N.A.
SENDENCE PROM D., BANKIER A.T., BORRAN S., BROWN D.,
CHURCHER C.M., CONNOR R., CONSET T., DEAR S., DEFULN K., PRASER R.
GENTLES S., LTR. G., MOTLE S., MOTLE T., ODELL C., PRASEO D.,
LOUIS S., LTR. G., MOTLE S., MOTLE T., ODELL C., PRASEO D.,
RANDERM M.M. SELES L., ROWLET N., SKILTON J., SRITH Y.,
MALSH S.Y., WHITEELD S., ROWLET N., SKILTON J., SRITH Y.,
SCHATTED (DES. 1.394) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER 1 1
SEQUENCE 797 AA; 91922 MW; 2D4D4AB9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POULAZI-1993 (REL 25, CRRATED)
01-NPR-1993 (REL 25, LAST REQUENCE UPDATE)
01-PER-1994 (REL 25, LAST ANDORATION UPDATE)
PROBABLE UNA DOLATERASE (EC 2.7.7.7) (PRAGMENT).
ACARICUS BITORQUIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 8; DB 1; Length
Pred. No. 4.71e+02;
0; Mismatches 0; In
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(GEP-BINDING PROTEIN 2) (FRAGMENT).

GEB-BROOPA, (PIG).

SULARYOTA, METANAGOA; CHORDATA; VERTEBRATA;

LITHERIA; ARTIONACTILA.

TETRAPODA;

MANMALIA;

Page 33

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Page 34
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AESULT 13

ID TWIL_TEAST STANDARD;
AC P1885;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 01-ROW-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE REPORTITICAL 12, PS DP POTEIN IN FLOS-PRO12 AND FLO1-PRO11 INTERGERIC
DE REGIONS.
GN YERSIZO AND YAROGOC.
GN YERSIZO AND YAROGOC.
GENAROTOTES CEREVISIAE (BAKER'S YEAST).
OC EUMAROTOTES CEREVISIAE (BAKER'S YEAST).
OC EUMAROTOTES TO SECREVISIAE (PAREZ).
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                                             RESERVATION OF DESCRIPTION OF DESCRI
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ID IB
AC P2
DT 01
DT 01
DT 01
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Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%;
Matches 8; Conservative
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P24853;
01-MAR-1992 (REL. 21, CREATED)
01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
01-FER-1995 (REL. 21, LAST SEQUENCE UPDATE)
101-FER-1995 (REL. 31, LAST SEQUENCE UPDATE)
118GULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 (ICPBP-2) (IBP-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1222 AAVTPAAG 1229
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439 AAVTPAAG 446
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264 AAPEPER 270
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NOW TER 51 51
SEQUENCE 51 AA; 5085 MW;
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                                                                                                                                                                                                                                          SERVINSES PROM N.A. (YMB212C).
STRAINSESSEC, A. 8972;
MEDILIE; 94378003, A. 9872;
JOHNSTON M. ANDREWS S., BRINKMAN R., COOPER J., DING H., DOVER J.,
DOHSTON M. ANDREWS S., BRINKMAN R., COOPER J., DING H., DOVER J.,
DOHSTON M. ANDREWS S., DULTON L., GEISEL C., KIRSTEN J.,
KCCAAN T., HILLER L., JERK M., JOHNSTON L., MASTON Y.,
MANNILER P., LOUIS E.J., MACH C., MARDIE E., MENEES S., MOUSEN L.,
MANNILE P., LOUIS E.J., MOHLDANN P., MATERSTON R., WILSON R.,
VICHNIL D., WILCOX L., WOHLDANN P., WATERSTON R., WILSON R.,
VAUDIN M.;
                                                                SERQUENCE FROM N.A. (YAROSOC).
STRAIN-S286C, A.8972;
BUSSET H., KENG T., STORMS R.K., YO D., ZHONG W., FOI
BARTON A.B. KARACK D.B., CLARK M.W.; DDBJ DATA BANKS
SUBHITTED (FEB-1994) TO EMBL/CENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                   IENCE 265:2077-2082(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160267
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3-1.
3-3.
3-3.
3-5.
3-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 7; DB 1; Length 51;
Pred. No. 5.98e+00;
0; Mismatches 0; Indel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 8: DB 1; Length 1480;
Pred. No. 4.71e-02;
0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4EC3AC9B CRC32;
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IN TYAL JUDAN
AC PO4437;
DT 11-AG-1897
DT 11-AG-1897
DT 01-AM-1900
DE 7-CELL RCCEP
GN 7CAL
GO EUTHARVA;
OC EU
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Op
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REQUENCE: 92109718

RA COLEMAN H.Z., PAN Y. C.E., ETHERTON T.D.;

RA COLEMAN H.Z., PAN Y. C.E., ETHERTON T.E. STIMULATE THE GROWTH

RAD CHAPTER SEEN SHOWN TO EITHEN INHIBIT ON STIMULATE THE GROWTH

ROUTHOUT OF THE SET OF THE GES ON CELL CHITCHE. THEY ALTER THE

CC. THE SHOULD THE THE THEY HAVE CELL SHEAKE RECEPTORS.

CC. T. SILLIARTY. BELIANGE TO THE INSULIN-LIKE GROWTH FACTOR BINDING

CC. T. SILLIARTY. BELIANGE TO THE INSULIN-LIKE GROWTH FACTOR BINDING

CC. T. SILLIARTY. BELIANGE TO THE INSULIN-LIKE GROWTH FACTOR BINDING

CC. T. SILLIARTY. BELIANGE TO THE INSULIN-LIKE GROWTH FACTOR BINDING

CC. PIR: JUDISJ. JUDISJ. TOP JUDISJ. SIEDING. PARTIAL.

DR PROSITER, PSOCREJ. TOP JUDISJ. SIEDING. PARTIAL.

DR PROSITER, PSOCREJ. TOP JUDISJ. SIEDING. PARTIAL.

RT NOW,—TER 21 23 23 23 50 SEQUENCE 23 AA. 2387 MF; SCSSBS4A CRC22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dec 21 09:28:29 1998
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Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%;
Matches 7; Conservative
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||||||
1126 SRKLPGT 1132
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P05942; 198 (REL. 10, CREATED)
01-PEP-1991 (REL. 17, LAST SEQUENCE UPDATE)
01-PEP-1995 (REL. 37, LAST ANNOTATION UPDATE)
MY051M LIGHT CHAIN 1, SLOW-TWITCH MUSCLE B/VENTRICULAR ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                          TCRA.
HONG SAPIENS (HUMAN).
EUDARYOTA: METAROA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALTA;
EUTHERIA; PRIMATES.
...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-C-3H; TISSUE-SPLZEN;
MEDLINE: 89057447.
COMEN A., BARTON P.J.R., ROBERT B.,
BUCKINGHAM M.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (FRAGMENT).
MTIJ OR MICIV.
MUS MUSCULUS (MOUSE).
EUKARYOTA: METAZOA: CHORDATA:
EUTHERIA: RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 RPPPAAP 21
|||||||
85 RPPPAAP 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9-AUG-1997 (REL. 05, CREATED)
3-AUG-1997 (REL. 05, LAST ESQUENCE UPDATE)
1-AUR-1990 (REL. 13, LAST ANNOVATION UPDATE)
1-AUR-1990 (REL. 13, LAST ANNOVATION V REGION (CTL-L17).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                              T-CELL RECEPTOR A V SEGMENT. D SEGMENT. J SEGMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 7; DB 1; Length 111;
Pred. No. 5.98e+00;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 7; DB 1; Length 23;
Pred. No. 5.98e+00;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GARNER I., ALONSO S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               139 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UB-08-951-733-20
                                                                                                                                                                                                                                                                                                                                                CYTOTOXIC T-LYMPHOCYTE
                                                                                                                                                                         ALPHA
                                                                                                                                                                         CHAIN V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                         REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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NON_TER 139 139
SEQUENCE 139 AA; 15441 MW; 8EAE2341 CRC32;
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Ouery Match 0.6%; Score 7; DB 1; Length 139; Best Local Similarity 100 0%; Pred. No. 5. 598+09. Matches 7; Conservative 0; Mismatches 0; Indels
4 LLGASVL 10
|||||||
|697 LLGASVL 703
                                                                     0,
                                                                     Scap
                                                                     0
```

01-FEB-1995 (REL. 11. CREATED)
01-FEB-1995 (REL. 11. LAST SEQUENCE UPDATE)
01-FOW-1997 (REL. 35. LAST ANNOTATION UPDATE)
ROMOPROTOCATECHNATE DEGRADATIVE OPERON REPRESOR.
HUCR OR HPAR.
BECHERICHIA COLI.
ESCHERICHIA COLI.
ESCHERIC STANDARD; PRT; 148 AA

SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAINS-C;
STRAINS-C;
RODER D.I., FANCETT T., COOPER R.A.;
RODL. GEN. GENET. 237:241-250(1993).

STOCHMENT PROM N.A.

E STOCHMENT PROM N.A.

E STOCHMENT PROM N.A.

E STOCHMENT PROM N.A.

E STOCHMENT PROM N.A.

LJ. BANTERIOL. 178:111:120(1996).

LJ. BANTERIOL. 178:111:120(1996).

C PATHAY HE COPERON.

C PATHAY HE COP

Ouery Match 0.0%; Score 7; DB 1; Length 148; Best Local Similarity 100.0%; Pred. No. 5:98e+00; Matches 7; Conservative 0; Mismatches 0; Indels 0; Indels ő Gaps

58 LRPSLTG 64

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9
21 09:28:29 1998
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CC SUBJULT AND 1-4 (114.38) -PERMIDISEDIONE AND 1-3 4-DIMPENSET-2-
CC SUBJULT CAPACISED THE CONDENSATION OF 1-MINOR (1.75) -REBITTL-
CC AMINO-2 A (114.38) -PERMIDIDISED TO 9 5-MINOR (1.75) -REBITTL-
CC AMINO-2 A (114.38) -PERMIDISED TO 9 5-MINOR (1.75) -REBITTL-
CC -1-CAPACISED TE LEADING 5-DIMPENSET -1-10-FEBITTL-
CC -1-CAPACISED TE STANDART -1-10-PEBITTL-
CC -1-CAPACISED THE A (1.10-PEBITTL-MINO) -5-MINO-2,6-DIMPENOXIPERINDINE.
CC -1-CAPACISED THAN -1-10-PEBITTL-
CC -1-CAPACISED THAN -1-10-P
```

88888888888888888

Gaps

Query Match 0.6%; Score 7; DB 1; Length 154; Best Local Similarity 100.0%; Pred. No. 5.98e+00; Matches 7; Conservative 0; Mismatches 0; Indels 0

0

å 28 ALLDGAR 34 ||||||| 124 ALLDGAR 130

LT 18
RR__SPIEX STANDARD: PRT; 155 AA.
PAJ342;
01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-FEE-1996 (REL. 3), LAST SEQUENCE UPDATE)
01-FEE-1996 (REL. 3), LAST ANNOVATION UPDATE)

RESULT TO SECOND DATE OF THE PROPERTY OF THE P SEOURNE FROM N.A.

LEM K.A., MANIART J.R.;
J. PRICOL. 29:500-505(1931).

-1- SIMILARTI, BELONGS TO THE STP PAMILY OF RIBOSOMAL PROTEINS.

BEBLI, LO7932; C470152;
-1- SEMILARTIE, PS00512; RIBOSOMAL, S7; 1.

RIBOSOMAL PROTEIN: CHICARPIAST;
SEOURNEE 153 AX. 17758 MR; 6958C1AB CRC12; PPROOTRA MATHA. SHLOROPLAST. DURANYON, PLANTA, PHYCOPHYTA; CHLOROPHYTA (GREEN ALGAE); DONJUGATOPHYCEAE; EYGNEMATALES; EYGNEMATINEAE; EYGNEMATACEAE

Overy Match 0.6%; Score 7; DB 1; Length 155; Best Local Similarity 100 0%; Pred. No. 5.98e+00; Matches 7; Conservative 0; Mismatches 0; Indels 0; Caps

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US-08-951-733-20.rsp

Page 39

ET 19

ROYC_PSALE STANDARD; PRT; 174 AA.

05:124;
01:40V-1997 (REL. 35, CREATED)
01:40V-1997 (REL. 35, LAST ASDUENCE UPDATE)
01:40V-1997 (REL. 35, LAST ASDUENCE UPDATE)
01:40V-1997 (REL. 35, LAST ANDVATION UPDATE)
UNCTION NUCLEASE ROYC) (ROLLIDAY UNCTION RESOLVASE ROYC).

SENDOMONAS AERUGINGEA. ROMANIOTA: GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND "SENDOMONADACEAE.

RESTRICTOR FROM N.A.

Query Match 0.6%; Best Local Similarity 100.0%; Matches 7; Conservative 164 GARRRGG 170 ||||||| 242 GARRRGG 248 Score 7; DB 1; Length 174; Pred. No. 5.98e+00; 0; Mismatches 0; Indels

..

Gaps

RESULT 20
ID YOPO_TEREN STANDARD: PRT: 182 AA.
AC P27474;
DT 01-AUG-1992 (REL. 23, CREATED)
DT 01-AUG-1992 (REL. 24, LAST ESQUENCE UPDATE)
DT 01-UUL-1993 (REL. 26, LAST ANNOTATION UPDATE)

Mon Dec 21 09:28:29 1998

Page 37

U8-08-951-733-20.xap

Page 38

YOJ_MYCTU STANDARD: PRT: 153 AA.
910530;
01-007-1996 (REL. 34, CREATED)
01-007-1996 (REL. 34, LAST ENGURNICE UPDATE)
01-007-1996 (REL. 34, LAST ENGURNICE UPDATE)
01-007-1996 (REL. 34, LAST ENGURNICE UPDATE)
11FOPHERICAL 16.8 ED PROTEIN CY427-196.

MYCOBACTERIUM TUBERCULOSIS. PRIXARYOTA; FIRMICUTES; ACTINOMYCETALES; MYCOBACTERIACEAE.

SENDENCE FROM N.A.
STALTS-SITALY
STALTS-SITALY
STALTS-SITALY
STALTS-SITALY
STALTS-SITALY
STALTS-SITALY
STALTS-SITALY
SUBLITITED (ARTS-SITAL)
SUBLITITED (ARTS-SITAL)
SUBLITITED (ARTS-SITAL)
SEDIENT STORS: STALTS-SITALY
SENDENCE 133 AN; 11819 MH; OFDJOCFC CRC32;

Query Match 0.6%; Best Local Similarity 100.0%; Matches 7; Conservative Score 7; DB 1; Length 153; Pred. No. 5.98e+00; 0; Mismatches 0; Indels 0 Gaps

27 RGAKKYL 33 {|||||| 113 RGAKNYL 119

RISB_MCCTU STANDARD: PRT; 154 AA.
P71655,
D1-80V-1997 (REL. 35, GERATED)
01-80V-1997 (REL. 35, LAST EXCURNICE UPDATE)
01-80V-1997 (REL. 35, LAST EXCURNICE UPDATE)
01-80V-1997 (REL. 35, LAST MANOVATION UPDATE)
01-80V-1997 (REL. 35, LAST ANNOVATION UPDATE)
01-80V-1997 (REL. 35, LAST ANNOVATION BETA CHAIR)
(LUDALINE SIVERIASE) (RIBOFLAVIN SYNTHASE BETA CHAIR).
MICHORACTERINA TURBERCULOSIS.
MICHORACTERINA TURBERCULOSIS.
ACTINOMICERALES; MICHORACTERIACEME.

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US-08-951-733-20.rsp

Page 41

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STARB DCCCLARKERS CCCCS YOPQ PROTEIN PRECURSOR. YOPQ OR YOP2O. YERSINIA ENTEROCOLITICA. PROLANTO PY. PROLANTOPA: CRACLICUTES; SCOTOBACTERIA; PACULTATIVELY ANALHOBIC RODS; PRIEROBACTERIACEAE.

CORNELIS G. ;

SIGNAL 1 24 POTENTIAL.
CHAIN 25 182 TOPO PROTEIN.
SEQUENCE 182 AA; 20828 MH; 2A32F684 CRC32;

Ouery Match 0.6%; Score 7; DB 1; Length 182; Best Local Similarity 100.0%; Pred. No. 5.98e+00. Matches 7; Conservative 0; Mismatches 0; Indels 0 Gaps

0

8

HA19_MOUSE STANDARD; PRT; 200 AA.

P14431;
01-JAN-1990 (REL. 13, CREATED)
01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
15-JUL-1990 (REL. 15, LAST ANOCHMICS UPDATE)
15-JUL-1990 (REL. 16, LAST ANOCHMICS UPDATE)

CHAIN PRECURSOR

NI-O9. MUS MOSCULOS (MOUSE). BUKARYOTA: METAKOA: CHORDATA: VERTEBRATA: TETRAPODA; MAMMALIA: EUTHERIA: RODENTIA.

Ouery Match 0.6%; Best Local Similarity 100.0%; Matches 7; Conservative

Score 7: DB 1: Length 199; Pred. No. 5.98e+00; O; Mismatches O; Indels

0

Gaps

0

INIT_MET 0 U 0426BB63 CRC32;

62 GSILSTL 68 ||||||| 856 GSILSTL 862

MLE_BAT STANDARD; PRT: 199 AA.

P16409;
01-MGC-1990 (REL. 15, CREATED)
01-MGC-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-FER-1996 (REL. 31, LAST SEQUENCE UPDATE)
MTGSIN LIGHT CHAIN 1, SLOW-TWITCH MUSCLE B_VENTRICULAR ISOPORM.
MTG10 RH.CLV.
MTG10 RH.CLV.
EURANGOTA, METALOA, CHORDATA; VERTEBRATA; TETRAPODA; NAMAALIA;
EUTHERIA; RODENTIA.

SEQUENCE FROM N.A. STRAIN-WISTAR; TISSUE-HEART VENTRICLE; MEDLINE; 90016857. DECUENCE FROM N.A.
TISSUES-HEARY VENTRICLE;
AUDILINE: 89240031.
ACNALLY E. BUTTRICK P., LEINAND L.,
ACNALLY E. BUTTRICK P., LEINAND L.,
AVILLEIC ACIDS RES. 17:2753-2767(1989).

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877777777888 HSSP: PO1899; 1ROC.

MGD: NGI:95938: H2-Q9.

PROSITE: P600390; IG_HC: PARTIAL.

HGC I: GLYCOPROTEIN: SIGNAL.

SIGNAL

22 >200

H-2 C

CHAIN

23 >200

H-2 C

461493EE CRC32;

97 GSLRTAQ 103 ||||||| 1116 GSLRTAQ 1122

DEF_MICH STANDARD; PRT: 216 AA.
P75527;
01-80V-1997 (REL. 35, CARATED)
01-80V-1997 (REL. 35, LAST ESQUENCE UPDATE)
01-80V-1997 (REL. 35, LAST ESQUENCE UPDATE)
01-80V-1997 (REL. 35, LAST ANNOTATION UPDATE
PROTECTION DEFORMITIASE (RC 3.5.1.31) (PDF) (FORMILMETHIONINE

COPLASMA PREDMORIAE. NORANTOTA: TENERICUTES; MOLLICUTES; MYCOPLASMA; MYCOPLASMATALES; COPLASMATACEAE.

L-METHIONINE.

1. CONCOR: REQUIRES AND BIND A FINC ION (BY SIMILARITY).

1. SUBUNIT: MONOMER (BY SIMILARITY).

22 22 22 20 200 A H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, OP ALPHA CIRLH:
EXTRACELUTIAR ALPHA-1.
EXTRACELUTIAR ALPHA-2.
BY SHILARITY.
POTENTIAL.

DOMAIN
DOMAIN
DISULFID
CARBOHYD
NON_TER
SEQUENCE 111 112 >200 12 185 107 200 23025 MH; (0.6%)

Query Match 0.6%; Best Local Similarity 100.0%; Matches 7; Conservative Score 7; DB 1; Length 200; Pred. No. 5.98e+00; 0; Nismatches 0; Indels 0 Gaps

SENDURSCE FROM N.A.
STRAINHAPOC 2014/ M129;
REPLINER 97105865.
RIMBELREICH R., BILBERT H., PIACENS H., PIRKL E., LI B.-C.,
RERREANN R.,
ROCLEIC ACIDS RES. 24:4420-4449(1996).
PUNCTION: REMOVES THE FORMYL GROUP FROM THE N-TERMINAL MET OF
INCREAL SENTRESIEED PROPERING (BY EMPILAINT).
I- CANALITIC ACTUTY: N-FORMYL-L-METHIONINE + H(2)0 = FORMATE +
I- CANALITIC ACTUTY: N-FORMYL-L-METHIONINE + H(2)0 = FORMATE +
I- CANALITIC ACTUTY: N-FORMYL-L-METHIONINE + H(2)0 = FORMATE +
I- CANALITIC ACTUTY: N-FORMYL-L-METHIONINE + H(2)0 = FORMATE +
I- CANALITIC ACTUTY: N-FORMYL-L-METHIONINE + H(2)0 = FORMATE +
I- CANALITIC ACTUTY: N-FORMYL-L-METHIONINE + H(2)0 = FORMATE +
I- CANALITIC ACTUTY: N-FORMYL-L-METHIONINE + H(2)0 = FORMATE +
I- CANALITIC ACTUTY: N-FORMYL-L-METHIONINE + H(2)0 = FORMATE +
I- CANALITIC ACTUTY: N-FORMYL-L-METHIONINE + H(2)0 = FORMATE +
I- CANALITIC ACTUTY: N-FORMYL-L-METHIONINE +
I- CANALITIC ACTUTY: N-FORMYL-METHIONINE +
I- CANALITIC ACTUTY: N-FORMYL-METHIONINE +
I- CANALITIC ACTUTY I- CANALITI

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U8-08-951-733-20

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SEQUENCE FROM N.A.
STRAIN-STRA

Page 43

FT ACT_SITE 179
FT METAL 182
SQ SEQUENCE 216 AA; 179 B1 182 E: 24592 MW; BY SIMILARITY. SINC (BY SIMILARITY). 9ED06092 CRC32;

Query Match 0.81, Scorre 7; DB 1; Length 216; Best Local Similarity 100.01; Pred. No. 5, 98e+00; Matches 7; Conservative 0; Mismatches 0; Indels 0; Indels 0 Gaps

٥

208 NPALPSD 214 |||||| 1142 NPALPSD 1148

TEGL_CAZEL STANDARD: PRT: 257 AA.

TEGL_CAZEL STANDARD: PRT: 257 AA.

P55336; 019405;
01-007-1996 (REL. 34, CREATED)
01-007-1996 (REL. 34, LASS ESQUENCE UPDATE)
01-007-1996 (REL. 35, LASS ANNOVATION UPDATE)
HTPOTHERICAL 28.7 KD PROTEIN F13E6.1 IN CHROMOSOME X.

#13E6.1. AENORHABDITIS ELEGANS. MKARYOTA; KETAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA

EDUTENCE FROM N.A.
STRAIN-BRESTOL N2:
GTRAIN-BRESTOL N2:
GTRAIN-BRESTO

Query Match 0.6%; Best Local Similarity 100.0%; Matches 7; Conservative Score 7; DB 1; Length 257; Pred. No. 5.98e+00; 0; Mismatches 0; Indels 0 Gaps

9

30 DAVVIEQ 36 ||||||| 810 DAVVIEQ 816

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RA PERIASANY M. MODADONAR R., KOWAR C., MARTIN B.J., SIDDIQII M.A.Q.:
RU NUCLEIC M.US RES J.7723-7734 (1989)
CC -1- SMEINIT: MOSEN 15 AN REMAKER OF 2 REMY CHAINS & 4 LIGHT CHAINS
CC -1- SMEINIT: MOSEN 15 AN REMAKER OF 2 REMY CHAINS & 4 LIGHT CHAINS
CC -1- SMEINIT: MOSEN 15 AN REMAKER OF 2 REMY CHAINS & 5 ALIGHT CHAINS
CC -1- SMEINIT: MOSEN 15 AN REMAKER OF 2 REMY CHAINT CHAIR REMAKER OF 2 REMY CHAINT CHAINT CHAIR REMAKER OF 2 REMY CHAINT CHAIR CHAINT CH

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US-08-951-733-20.rsp

Page 45

Mon Dec 21 09:28:29 1998

US-08-951-733-20.rsp

Page 46

III
SECTEMOR PROM N.A.
SECTEMOR PROM N.A.
TISSUE-LIVER;
HEDLINE; 3144118.
HEDLINE; 3144118.
HEDLINE; 314418.
H. ARTON H.J. ARAO H., INOUZ K.;
L. BIOCHEM, J. 306:437-443(1995).

TAKAHASHI

; s

SEQUENCE FROM N.A.
DENG H.X., RENTATI A., SIDDIQUE T.;
COMMITTED (FEB-1995) TO EMBL/GENBANK/DDBJ

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BOYER H.W.;
GENE 12:287-299(1980).
                                                                                                                                  VIRIDAE; DS-DNA NONENVELOPED
                                                                                                           EQUENCE FROM N.A.
STRAIN-GOMEN;
SIZDLINE; 81237792.
DIJUEMA R., DEKKER B.M.M.,
                                                                                                                                   VIRUSES;
                                                                                                                                   ADENOVIRIDAE; MASTADENOVIRUSES
                                                                                                             ä
                                                                                                             WAARD A., MAAT J.,
```

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

TOSALIN-GRIDBELLINAGA K.;

A TOSALIN-GRIDBELLINAGA K.;

L. TIDERI RES.

TO PROCTION: TRANS-ACTIVATES EARLY VIRAL PROMOTERS AND SOME CELLULAR PROMOTERS. THE SEPACE OF THE SERVICE OF THE SEALY 6.3

L. TIDERI RES.

RY WARLANT AND CUT-101.

RY MARLANT AND CUT-101.

RY MARCHAIL SUITS M., ARAI H., INOUE K., YONOTA T., FUNUO Y.,

RA MARCHAIL SUITS M., ARAI H., INOUE K., YONOTA T., FUNUO Y.,

RA MARCHAIL SUITS M., ARAI H., INOUE K., YONOTA T., FUNUO Y.,

RA MARCHAIL SUITS M., ARAI H., INOUE K., YONOTA T., FUNUO Y.,

RA MARCHAIL SUITS M., ARAI H., INOUE K., YONOTA T., FUNUO Y.,

REPARATE MARCHAILES.

CC -1 FUNCTION BENEGAL MARCHAIL RECURSAIN MITH ISOLATED

CC -1 DISEASE DEFECTS IN TIPPI ARE THE CAUSE OF ATAXIA WITH ISOLATED

CC -1 SIMILIATIT: NO CELLULAR RETINALDRIDE-SINDING PROTEIN.

CC -1 S

BETWEEN

Query Match

Best Local Similarity 100.0%;
Matches 7; Conservative 178 LLCSLCY 184 ||||||||| 862 LLCSLCY 868 Score 7; DB 1; Length 261; Pred. No. 5.98e+00; 0; Mismatches 0; Indels 0 Gaps 0

B

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  2
                                                                                                               ROMO SADIENS (UDMAN).
EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
EUTHERIA: PRIMATES.
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US-08-951-733-20.rsp
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RESULT 26

TEP__HUMAN STANDARD; PRT; 278 AA.

TO 749591; 1996 (REL. 33, CREATED)

TO 1-FES-1996 (REL. 33, CREATED)

TO 1-FCT-1996 (REL. 34, LAST SECOTENCE UPDATE)

DT 01-FCT-1996 (REL. 34, LAST SECOTENCE (ALPHA-TEF).

STANDAY-TOCOCHERCO TRANSFER FROTEIN (ALPHA-TEF).

STANDAY-TOCOCHERCO TRANSFER FROTEIN (ALPHA-TEF).

STANDAY-TOCOCHERCO TRANSFER FROTEIN (ALPHA-TEF).

SECONDOTAL PREMISE. CHORDATA: VERTEBRATA: TETRAPO

CEUTHERIA, PREMISE.
```

SEULY 27

PA25K_STRCC STANDARD; PRT; 278 AA.

PA35K_STRCC STANDARD; PRACTICE STANDARD; PROMATOR; PREMICTORS, COCCI, STREPPOCOCCABAE.

片

36 REAGVPL 42 ||||||| 230 REAGVPL 236

Query Match
Best Local Similarity 100.0%;
Matches 7; Conservative

Score 7; DB 1; Length 278; Pred. No. 5.98e+00; O; Mismatches 0; Indels

Indels

0

Gaps

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US-08-951-733-20.rsp

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Query Match

Best Local Similarity 100.0%;
Natches 7; Conservative
                                                                                                                                                                 1. FUNCTION: INTERACTS WITH DNA, TO DISASSEMBLE A PROTEIN COMPLEX AND THE AREA MADE AND ADMINISTRATIVE THE STRUCTURE OF THE ATENDAMES JOINTLY.

1. SAMILARITY, TO OFFICE AREA STRUCTURE OF DAMA, AND TO EUMARITOTIC DAMA-LIKE PROTEINS.

EMB. 109001 G1552189: -.

EMBLE 1990015 DNA, REPLICATION: HEAT SHOCK.
DOMAIN 89 110 GLY-REIGH.

DOMAIN 89 110 GLY-REIGH.

DOMAIN 89 110 GLY-REIGH.

DOMAIN 89 110 GLY-REIGH.
129 VVSPARP 135
|||||||
294 VVSPARP 300
                                                                                    Score 7; DB 1; Length 307;
Pred. No. 5.98e+00;
0; Mismatches 0; Indels
                                                                                           0
                                                                                           Caps
                                                                                           0
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A PRESERVE SELECTER S

SINILARITI BELONG T BOTELNS T BOTELNS TO 310832 T TAMESPERATE TAMEPORT TAMESPER 10 60 TAMESPER 10 60 TAMESPER 10 61 TAMESPER 10 11 TAMESPER 10 11 TAMESPER 10 11

77; G310632; ...
NABE; TTANBSORT.
40 60
61 81
94 114
134 114
134 114
134 119
222 242
246 266
278 AA: 29705 p

POTENTIAL

SEQUENCE FROM N.A.
STRAIN-PK488;
MEDLINE; 95012638.
KOLENBRANDER P.E.
INFECT. IMMUN. 62:4

:4469-4480(1994).

ION: INTEG

SRAL MEMBRANE PROTEIN (PROBABLE). ABC-3 SUBPAMILY OP INTEGRAL MEMBRANE

δõ F

ESCHERICHIA COLI. PROMANTOTA: GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; ENTEROBACTERIACEAE:

G. III, MAYHEW G.F., PERNA N.T., EMBL/GENBANK/DDBJ DATA BANKS. STUMPE S., TEWES R., SCHMID R., EMBL/GENBANK/DDBJ DATA BANKS. BAKKER GLASNER

SEQUENCE FROM N.A.

KEDLINE; 9705(12).

KANEKO T., SATO S., KOZANI H., TANAKA A., ASAMIZU E., KAKAMURA Y.,

KANEKO T., SATO S., KOZANI H., SOGJURA M., SASAMOTO S., KIUURA T.,

KITUJIKA N., HIROSAWA M., SUGJURA M., SASAMOTO S., KIUURA T.,

KESOUCHI T., MATSUDO A., TURAKI A., MAKAJAKI N., KRHOD K.,

CKUURURA S., SILEPO S., TAKEUCHI C., WADA T., WATANABE A.,

YAMADA M., TASUDA M., TASATA S.;

DAN RES. 3:103-116(1955).

BEULT 28

BULL SYN3 STANDARD: PRT: 307 AA.

C P73097:

T 01-MOV-1997 (REL. 35, CREATED)
T 01-MOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
T 01-MOV-1997 (REL. 35, LAST ANDOTATION UPDATE)
T 01-MOV-1997 (REL. 35, LAST ANDOTATION UPDATE)
T 01-MOV-1997 (REL. 35, LAST ANDOTATION UPDATE)

BULL PROTEIN
DRAJ PROTEIN
BULL STANLIN CONCENTION
STRENDOCTORIA GRACILICUTES; OXTROGORDACTERIA;
C PROGRAFOTA GRACILICUTES;
C PROG

Query Match 0.6%; Best Local Similarity 100.0%; Matches 7; Conservative

Score 7; DB 1; Length 278; Pred. No. 5.98e+00; O; Mismatches 0; Indels

indels 0

Gaps

9

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232 GASVLGL 238 |||||||| 699 GASVLGL 705

RESULT 29

ID SAPE_SCOLL STANDARD: PRT: 321 A.

AC Q47632; p768214.

D7 01-NOV-1997 (REL. 35; CLEATED)

D7 01-NOV-1997 (REL. 35; LAST SEQUENCE UPDATE)

D7 01-NOV-1997 (REL. 35; LAST SEQUENCE UPDATE)

D7 01-NOV-1997 (REL. 35; LAST SAROTATION UPDATE)

D8 PETITIDE TANNSPORT SYSTEM PERMEASE PROTEIN SAPE

B SEQUENCE PROM N. A.

RE SEQUENCE FROM SEQUENCE FROM N.A.
STRAIN-41210 FROM N.A.
ALDA N., BURTUCHI T.,
ALDA N., BABA T., FUJITA K., HAYASHI K., HONJO A., HORTUCHI T.,
ALDA N., BABA T., ELOHO K., ISONO S., ITOH T., KANAI K., MAKINO K.,
KASHIPOTO K., KINDA T., HIJOHO S., KINDANA H., KOTOHOTA K., MAKANDA T.,
MASHANOTO H., HISHO Y., OSHIMA T., SAITO N., SAMPEI G., SEKI T.,
MASHANOTO H., TAKENOTO K., WADA C., YAMANOTO T., TANO K.;
TAGANI H., TAKENOTO K., WADA C., YAMANOTO T., TANO K.;

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PLAYS A NOLE IN THE RESISTANCE TO ANTINICROBILL PEPTIDES.
SUBCELLULAR LOCATION: INTEGRAL MEMBRARE PROTEIN: INNER MEMBRARE
(POTENTIAL)
SIMILARITY: MYTEGRAL MEMBRARE CONSONERTS OF OTHER BINDINGPROTEIN DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE OPPBC

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Query Match 0.6%;
Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                        LT 30

SADE_SALTY STANDARD; PRT; 321 AA.

P35668;
01.JWR-1994 (REL. 29, CREATED)
01.JWR-1994 (REL. 29, LAST SCOURACE UPDATE)
01.FRE-1994 (REL. 21, LAST SCOURACE UPDATE)
PEPIDE TRANSPORT SYSTEM PERMEASE PROTEIN SAPB.
                                                                                                                                                                                                                                                              83 LAFGFAL 89
|||||||
119 LAFGFAL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBHITTED (DEC-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.

- FUNCTION: INVOLVED IN A PEFFIDE INTAKE TRANSPORT SYSTEM THAT

- PLAYS A ROLE IN THE RESIGNACE TO ANYILICROSIAL PEFFIDES.

- SUBCELUTAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER HEMBRANE
                                                                                       LAONELLA TYPHIMURIUM.
DARYOTA: GBACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS
TEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
SIMILARITY: 1
PROTEIN-DEPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-
DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE OPPBC
                                                                                                                                                                                                                                                                                                                 Score 7: DB 1; Length 321;
Pred. No. 5.98e+00;
0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FALSE_NEG.
RANE; INNER MEMBRANE
                                                                                                                                                                                                                                                                                                                 Gaps
6
                                                                                                                                                                                                                                                                                                                   0
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SÉÓMENCE FROM N.A.
STRAIN-10788;
FEDLINE: 94038887
FARRA-LOPEZ C., BARE N.T., GROISMAN E.A.;
MED J. 12:4053-4062(1993).
-I- FUNCTION: INVOLVED IN A PEPTIDE INTAKE TRANSPORT SYSTEM
          THAT
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Dec 21 09:28:29 1998

US-08-951-733-20.rsp

STRAIN-C5781/10; MEDILHE: 66135949. DEVLIN J.J., WEISS E.H., PAULSON M., FLAVELL R.A.; EMBO J. 4:3203-3207(1985).

ESCUENCE FROM N.A. TURNING-538L/JO ANDERS G.I., SEEDONN D.H., CALVIN S., ALLEM H., FLAVELI R.A.: (A.DECK. MED. 165:1358-1370(1987).

PROMERCE FROM N.A.
SENDLIES 9025579
STEINSTE M., MOORE K.W., FRELINGER J.G.,
BOTSE E.A., EGOD L.;
LEL 25:683-692(1981).

SHER B.T., SHEN F.W.,

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287 ASRSLPL 293 ||||||| 250 ASRSLPL 256

Sal Civil Sal Ci

TIDAL_SCHOO STANDARD, PRT; 330 AA.

Q10114;
Q10214;
Q10214;
Q10214;
Q10217;
Q1027-1996 (REL. 34, CERATED)
Q1-007-1997 (REL. 35, LAST ANNOTATION UPDATE),
Q1-007-1997 (REL. 35, LAST ANNOTATION UPDATE),
Q1-007-1997 (REL. 35, LAST ANNOTATION UPDATE),
Q10407-1004 (REL. 34, LET ANNOTATION UPDATE),
Q10407-1004 (REL. 34, LET ANNOTATION UPDATE),
Q10407-1004 (REL. 34, LET ANNOTATION),
Q10407-1004 (REL. 34, LET ANNO

Query Match 0.6%; Score 7; DB 1; Length 330; Best Local Similarity 100.0%; Pred. No. 5.98e+00; Matches 7; Conservative 0; Mismatches 0; Indels

0

Cape

SEQUENCE FROM N.A.

STRAIN-73: CHURCHER C.M., BARRELL B.G., BAJANDREAM M.A., WALSH S.V.;
DEVLIN K., CHURCHER C.M., BARRELL B.G., BAJANDREAM M.A., WALSH S.V.;
DEVLIN K., CHURCHER C.M., BARRELL B.G., BAJANDREAM M.A., WALSH S.V.;
DEVLIN K., CHURCHER C.M., BARRELL B.G., BAJANDREAM M.A., WALSH S.V.;
DEVLIN K., SEDONES C.M., SEDONES C.M., BAJANDREAM M.A., WALSH S.V.;
DEVLIN K., SEDONES C.M., BAJANDREAM M.A., WALSH S.V.;
DEVLIN K., SEDONES C.M., SED

220 QLLRQHS 226 ||||||| 472 QLLRQHS 478

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C PROTEIN-V....

C SUBPALIZ.
C
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overy Match 0.6%; Score 7; DB 1; Length 329;
Best Local Similarity 100.0%; Pred. No. 5.98++09;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 LAFGFAL 89
||||||
119 LAFGFAL 125
                                                                                                                                                                                                                                                                                                                                   CENTLES 6., CHURCHER C.M., BARRELL B.G., RAJANDRAM K.A., WALSH S.V.;
SUBMITTED (UL.1995) TO SEBL/CHEBNAKK/DDD DATA BANGS.
1- SHALARITY: STRONG, TO PRAST THROSSC.
EMBL. SEOL43: 01053799;
1- SEAUCHER C.M. SEOLEM, SEO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAZ, 31.

TAZE_SCEPO STANDARD; PRT; 129 AA.

090704;
01-80V-1995 (REL. 32, CREATED)
01-80V-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-80V-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-80V-1995 (REL. 32, LAST SEQUENCE UPDATE)
HTPOTHETICAL 56.7 ND PROTEIN C2F7.14C IN CHRONOSCHE
SPACEF7.14C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
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RP SEQUENCE OF 292-334 FROM N.A.

RP SEQUENCE OF 292-334 FROM N.A.

RP MULKER N. LEBIS E.D., HOOD L.E., STROTNOWSKI I.;

RA UULKER N. LEBIS E.D., HOOD L.E., STROTNOWSKI I.;

RA UULKER N. LEBIS E.D., HOOD L.E., STROTNOWSKI I.;

RA UULKER N. LEBIS E.D., HOOD L.E., STROTNOWSKI I.;

RA UULKER N. LEBIS E.D., HOOD L.E., STROTNOWSKI I.;

RA UULKER N. LEBIS E.D., HOOD L.E., STROTNOWSKI I.;

REDO J. 9:1819-3487(1290)

C. -- STROTNOWS RESTERN N. THE PRESENTATION OF POREIGN ANTIGENS TO COMPANY N. LEBIS E.D.

REDGL: A01210, E273947; JONED.

REDGL: A01210, E273947; JAL_INIT.

REDGL: A01210, A01210, LAULEC, L.

REDGL: A01210, A01210, L.

REDGL: A01210
Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H-2 CLASS I HISTOCOMPATIBILITY ANTIGEM, OF ALPHA CIRLIN:
EXTRACELIULAR ALPHA-1.
EXTRACELIULAR ALPHA-2.
EXTRACELIULAR ALPHA-3.
CONNECTING PEPTIDE.
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RP "

BALT_MOOSE STANDARD: PRT: 334 AA.
p14439:
01-JAN-1990 (REL. 13, CREATED)
01-JAN-1990 (REL. 13, CREATED)
01-HOV-1997 (REL. 15, LAST ANNOTATION UPDATE)
H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, 07 ALPHA
(QA-2 ANTIGEN).

MUS MUSCULUS (MODE). BURANYOTA, HETAMOA, CHORDATA, VERTEBRATA; TETRAPODA; MAMGALIA; EUTHERIA; RODENTIA.

SEQUENCE PROM N.A.

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Best Local Similarity 100.0%; Pred. No. 5.98e+00; Matches 7; Conservative 0; Mismatches 0; Indels 0;

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Gaps

0

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Page 53
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Dec 21 09:28:29 1998
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(GALACTOWALDENASE).

AEOSPIRILUM BRASILENSE. PLASHID MEGAPLANID P90. PROKANYON, GRACILICUTES: SCOTOBACTERIA; AEROBIC, MOTILE, HELICAL AND/OR VIBRIOID

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PATOS, TEAST STANDARD: PRT: 347 AA.

PATOS, 196 (REL. 33, CREATED)

10. FEB. 196 (REL. 33, LAST SEQUENCE UPDATE)

10. CCT. 196 (REL. 34, LAST ANNOVATION UPDATE)

10. CCT. 196 (REL. 34, LAST ANNOVATION UPDATE)

PETILO ROTELN.

PETILO ROTELN.

SECONMONTEDS CREVISINE (MAKEY'S PEAST),

ENGAROMETES CREVISINE (MAKEY'S PEAST),

ENGAROMETES CREVISINE (MAKEY'S PEAST).
                                                                                                                                                                                                                                                                     97 GSLRTAQ 103
|||||||
1116 GSLRTAQ 1122
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SEQUENCE FROM N.A.

CUI I., MASON T.;

CUI II., MASON T.;

CUNITTED (OCT-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.

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342 GGSASRS 348 |||||||| 247 GGSASRS 253

TIAN 36

TIAN PART STANDARD; PRT; 355 AA.

P21109;
01-PMT-1991 (REL. 17, CREATED)
01-PMT-1992 (REL. 25, LAST RESOURCE UPDATE)
01-WMT-1992 (REL. 25, LAST RESOURCE UPDATE)
01-WMT-1997 (REL. 25, LAST RESOURCE UPDATE)
11-REA APETIMITY HITERLEVALIN-8 RECEPTOR A (II-8R A) (CXCR-1).

RICAROTORA METANADA (RABBIT)
RICAROTORA MANDALLA;
RICHAROTORA METANADA (RABBIT)
RICHAROTORA METANADA (RABBIT)

Query Match 0.6%; Best Local Similarity 100.0%; Matches 7; Conservative

Score 7; DB 1; Length 348; Pred. No. 5.98e+00; 0; Mismatches 0; Indels

Indels

0

Caps

0

BY SECURNIC FROM M. A.

RE STRAIL-BP, ANGC 39145;

RE MEDILIRE, 9459180.

RA MEDILIRE, 9459180.

RA DET TROCH P., KELIZES V., VANDERLEYDEN J.;

RA DET 144:134-144(1994).

CC -1- CATALITIC ACTIVITY: UDP-GLUCOSE = UDP-GALACTOSE.

C-1- CATALITY CATIVITY: UDP-GLUCOSE = UDP-GALACTOSE.

CC -1- PATHWALTY. EXHOPLISACCHARIDE AND LIPOPOLYSACCHARIDE BIOSYNTHETIC

CC -1- PATHWALTY. NITH OTHER GALACTOWALDENASES FROM EUKANYOTIC AND

CC -1- PROMANOTIC ORIGINATIONE METABOLISM: PLASMID.

RM ISOMERASE, NAD. GALACTOSE METABOLISM: PLASMID.

RM ISOMERASE, NAD. GALACTOSE METABOLISM: PLASMID.

SO SEQUENCE 348 AA; 35700 MM; 398DOSED CRC12;

MITOCHONDRION.
SEQUENCE 347 AA; 39812 MW; 85A9097F CRC32;

ouery Match 0.6%; Score 7; DB 1; Length 347; Best Local Similarity 100 0%; Pred. No. 5.98e+00; Matches 7; Conservative 0; Mismatches 0; Indels 0 Caps

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RESULT
DT 015
DT 01
DT 01
DETOBLACOBE STANDARD: PRT: 348 AA.
($508)
01:MOV-1997 (REL. 35, CREATED)
01:MOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01:MOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01:MOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01:MOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
UDP-GLUCOSE 4-EPIMERASE (REC 5.1.3.2) (UDP-GALACTOSE 4-EPIMERASE)
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MEDLINE; 91056034. THOMAS K.M., PYUN H.Y., NAVARRO J.; J., BIOL. CHEM. 265:20061-20064(1990)

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

TISSUE-SECTION PRICE.

MEDIATE: 92148149.

LEE J., KUANG W.-J., RICE G.C., WOOD W.I.;

LEE J., KUANG W.-J., RICE G

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0
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Page 55
      8
   Dec 21 09:28:29 1996
                                                                                                                                                                                                        SEOCHEME PROM N.A.

KEDLINE; 9137894.

KEDLINE; 9137894.

LIMAN S., CERAND N.P., CERNED C., CERNETTI D.P.;

BIOCHEM: BIOPHIS. RES. COMMUN. 179:784-789(1991).
                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=ALBINO; TISSUE=NEUTROPHILS;
      US-08-951-733-20.rsp
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Db 336 LTRHRVT 342
|||||||
Qy 1104 LTRHRVT 1110
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REPORTED FROM N.A.

REPORTED (1.1.-1955) TO EMBL/GERBANT/DDSJ DATA BANKS.

RL SUBMITTED (1.1.-1955) TO EMBL/GERBANT/DDSJ DATA BANKS.

RL SUBMITTED (1.1.-1955) TO EMBL/GERBANT/DDSJ (1.0.-12.) THE ACTIVITY OF CITY PROCTION. RECEPTOR 15 MEDIATED SI G-S PROTEIN THAT SETTICULATES ADMITTATE CHASE. THE SUBSEQUERY BASE IN THAT SETTICATE CAMP IS CHESCALL THE RELAXING EFFECT OF THIS RECEPTOR ON SMOOTH COMMISCALL.

CONTROLLED LOCATION: INTEGRAL MEMBRANE PROTEIN.

CONTROLLED LOCATION: INTEGRAL MEMBRANE PROTEIN COUPLED RECEPTORS.

CONTROLLED LOCATION: INTEGRAL MEMBRANE PROTEIN COUPLED RECEPTORS.

CONTROLLED LOCATION: INTEGRAL MEMBRANE PROTEIN COUPLED RECEPTORS.

CONTROLLED LOCATION CONTROLLED COUPLED RECEPTORS.

RECENTATION CONTROLLED CONTROLLED CONTROLLED COUPLED RECEPTORS.

RECENTATION CONTROLLED CONTROLLED CONTROLLED COUPLED RECEPTORS.

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RECENTATION CONTROLLED CONT
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Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE PROM N.A.
TISSUE-PLACENTA;
MEDILHE: 945581T . J., PEPPERL D.J., PIERCE K.L., BOGARDUS A.M.,
REAM V.M., BAILEY T.J., PEPPERL D.J., PIERCE K.M., WOODWARD D.F., GIL D.W.;
MDL. PHARMACOL, 46:213-220(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PREZ_HUMAN STANDARD; PRT; 356 AA.

PA115;

PA115;

PA115;

PA115;

PA115;

PA115;

PA115;

PA116;

PA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146
204
287
355 AA;
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204 R
288 DJ
; 40622 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HA -> QS (IN REF. 2).

H -> C (IN REF. 2).

DI -> EL (IN REF. 2).

M: 2EB3947D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 7; DB 1; Length 355;
Pred. No. 5.98e+00;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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)Y SIMILARITY.)LLPALTMPIWAVSKEKGWIPG -> >APCPDHAYLGRIQGKRLDPR (IN REF. 2).

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CAPROPEIN
DOM IN
TRANSPER
TRAN
     358 J
     3
187 B
150 A
Y SIMILARITY.
-> R (IN REF. 2).
8EP7D003 CRC32;
                                                                                                                                                                               (TRACELLULAR (POTENTIAL).
(POTENTIAL).
(TOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INE: GLYCOPROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                               AR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
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Query Match 0.6%; Best Local Similarity 100.0%; Matches 7; Conservative 245 PGARRRG 251 ||||||| 241 PGARRRG 247 Score 7; DB 1; Length 358; Pred. No. 5.98e+00; 0; Mismatches 0; Indels 0 Gaps

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DE TERE_HUMAN STANDARD, PRT; 375 AA.

C 999712 (39446; 00564)
7 01-NOV-1997 (REL. 35, CREATED)
77 01-NOV-1997 (REL. 35, CREATED)
77 15-JUL-1998 (REL. 36, LAST ANNOTATE)
78 170-SENSITIVE INVALOR RECTIFIER PORISON OFDATE)
82 CHANNEL, HWARDLY RECTIFIER, SUPPARILY J, HEMBER 15 (POTASSITM PROTASSITM PROPASSITM PROPASSITM SUPPARILY J, HEMBER 15) (INWARD PROCESSIT (ROLAN)
83 ENGLISHER (ROLAN)
84 ENGRAPHER (ROLAN)
85 ENGRAPHER (ROLAN)
86 ENGRAPHER (ROLAN)
87 ENGRAPHER (ROLAN)
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88 ENGRAPHER (ROLAN)
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80 ENGRAPHER (ROLAN)
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88 ENGRAPHER (ROLAN)
89 ENGRAPHER (ROLAN)
89 ENGRAPHER (ROLAN)
80 ENGRAPHER (ROLAN

OURNE FROM N.A.
SSUE-KINNEY:
UCR M.E. PISEST.N., BOCK J.H., SLIGHTON J.L.,
UCR M.E. PISEST.N., BOCK J.H., SLIGHTON J.L.,
BIOL. CHEM. 271:586-593(1997).

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Mon 8 21 09:28:29

GAL1_STRLI P13227; STANDARD; PRT; 397 AA.

1. PROGREMOTE.

1. PROGREMOTE.

1. SINILARITY. TO OTHER PROMETER OF CALACTOSE METHABOLISM (LEIGHE PROMETER).

1. SINILARITY. TO OTHER PROMETER DEPTHE SERVE THE SHOWN IN POSITIONS 49

10 61, 181 TO 244, AND 288 TO 310 DE TO PRAMESHIPTS.

10 61, 181 TO 244, AND 288 TO 310 DE TO PRAMESHIPTS.

12 CONTION. SERVICE CONFLICT 181 ATP (POPENTIAL)

ALBHOYA-VERRERR -> PCRTRSNB-PCANDG

REGULAR TILL REGULA-VERRELLAVOTREVERSIS

BGEVERRAGGERGALLGVDAL -> BACTPSSSTRANSP

GENERRAGGERGALLGVDAL -> BACTPSSSTRANSP

GENERRAGGERGALLGVDAL -> BACTPSSSTRANSP

GENERRAGGERGALLGVDAL -> BACTPSSSTRANSP

GENERRAGGERGALLGVDAL -> GATTALASAAL

GENERRAGGERGALSSERDISTANSPELDIAVOTALASAAL

GO-NITCALASSERJAATPALRELPHILLPRAGPGREEGFG

G-> NITCALASSERJAATPALRELPHILLPRAGPGREEGFG

SEQUENCE 397 AA; CONFLICT 289 41984 MW; 330 LRGPR (IN REF. 1) 65555569 CRC32:

Query Match 0.6%; Best Local Similarity 100.0%; Matches 7; Conservative Score 7: DB 1; Length 397; Pred. No. 5.98e+00; O; Mismatches O; Indels 0

Gaps

-ANN-1990 (REL. 13, CREATED)
-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
LACTORINASE (EC 2.7.1.6).

REPTOMYCES LIVIDANS. ROKARYOTA; FIRMICUTES; ACTINOMYCETALES; STREPTOMYCETACEAE

ESOURMCE FROM N.A.
MEDILHE: 88086869.
NAMMS C.W., FORMWALD J.A., SCHMIDT F.J., ROSEMBERG M., BRANNER M.E.;
DACHS C.W., FORMWALD J.A., SCHMIDT F.J., ROSEMBERG M., BRANNER M.E.;
A., BACTERIOL. 170:203-212(1988).

DENTIFICATION OF PROBABLE FRAMESHIFTS.

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STANDARD; PRT;

402 24.

CA21_BOVIN P02465; 21-JUL-1986 21-JUL-1986 01-NOV-1995 TL-1986 (REL. 01, CREATED) TL-1986 (REL. 01, LAST SEQUENCE UPDATE) VV-1995 (REL. 32, LAST ANNOTATION UPDATE) OREN ALPHA 2(1) CHAIN (FRAGHENT).

BOS TAURUS (BOVINE). EURANCOTA, METALOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUPHERIA; ARTIODACTYLA.

SENDURKCE OF 1-19.
MEDLINE: 75036115.
FIETEER P.P., BREITKREUTE D., KUEHN K.;
FIETEER P.P., BREITKREUTE D., KUEHN K.;
FIGNOHIM. BIOPEYS. ACTA 365:305-310(1974).

SEQUENCE OF 16-336, AND REVISION. MEDDLHE: 76091874. FIETZEK P. P., REXRODT F.W.; EUR. J. BIOCHEM. 59:113-118(1975).

SEQUENCE OF 337-366. MEDLINE: 75008198. PIETLEK P.P., FURTHWAYR H., KUZHN K.; EUR. J. BIOCHEM. 47:257-261(1974).

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US-08-951-733-20.rsp

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Page 57

OURNER PROM N.A.
INDEX. PROM N.A.
IND. H., SETI N., MAASE T., SUERKI E., MONDRA N., ORARA O.,
ITON H., SATANI Y., EXI T., MURAKANI Y., SAITO T., ICHIRAWA H.,

BMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

RECURIES PROM N.

RECURIES PROGRAMA CA., KORN B., YASPO M.-L., POUTSKA A.,

RECURIES P. GIEZPALA CA., KORN B., YASPO M.-L., POUTSKA A.,

RA COSSET P. GIEZPALA CA., KORN B., YASPO M.-L., POUTSKA A.,

RA COSSET P. GIEZPALA CA.,

RA COSSET P. GIEZPALA CA.,

CC C. GRAYER TENDARCT YO ALLON POTASSITH ARE CHARACTERIZED BY A

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CONCEMPANT OF CO

CONFLICT CONFLICT CONFLICT SEQUENCE 98 235 245 375 AA; AL (POTENTIAL).

MI (POTENTIAL).

Query Match 0.6%; Best Local Similarity 100.0%; Matches 7; Conservative Score 7: DB 1; Length 375; Pred. No. 5.98e+00; 0; Mismatches 0; Indels 0

Caps

260 ETSPLRD 266 ||||||| 804 ETSPLRD 810

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Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%;
Matches 7; Conservative
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SCIENCE 365:2077-2002(1994).

SCIENCE 105:2077-2002(1994).

EMBL; U10397:650655: -

PIR: 546759; 946759.

HTPOTHETICAL PROTEIN.

SEQUENCE 465 AA: 51115 MY; 6848
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HLYD_ECOLI
P06739;
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|}|||||
1079 GAKGAAG 1085
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STRAINSHESS PRESTER / NIH: TISSUE-EMBRYO!
HORFIG K. BARNIGOL-WAYANDE S., BARNIGOL U., HILSCHMAN N.;
SUBMITTED (NOV-1997) TO SEEL/CERBANK/DBS DAYA BANES.

FUNCTION: HAS A DNA BINDING PROPERTY. THE POTEWILK EF-NAMD
FRACTIONS TOGETHER WITH THE KOLIC REGION MAY REGULATE THE
DNA-BINDING PUNCTION OF THE PROTEIN OF SEMILATITY).

FUNCTIONS FOR HOMAL-BINDING: EF-THAND; AMACIDIC REGION.

FUNCTIONS FOR HOMAL-BINDING: EF-THAND; AMACIDIC REGION.

FUNCTIONAL COCATION: SECRETED (FOTEWHIAL).

SELFICATION OF THE REP-HAND CALCIUM BINDING PROTEINS. BELONGS TO
BELLICATION: SELFICATION.
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NON_TER 402
SEQUENCE 402 AA;
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PRIDLINE; 94378003.

JOHNSTON M. ANDREWS S., BRINDMAN R., COOPER J., DING H., DOVER J.,

DO S., FAVELLO A., FULTON L., GATTUNG S., GEISEL C., KIRSTEN J.,

KUCLAM T., HILLER L., JURE M., JOHNSTON L., LANGSTON T.,

KATREILLE P., LOUIS E.J., MACRI C., MANDIS E., MENZESS S., MOGER L.,

HAN M., RIFKIN L., RILES L., ST PETER M., TREANARIS S., VAUGHAN K.,

HIGHANT D., HILCOX L., WOLLDMAN P., WATERSTON R., MILSON R.,

KITCHAN M., ELEVIN C., ST., PETER M., TREANARIS S., MADENAN K.,

RIGHANT D., WILCOX L., WOLLDMAN P., WATERSTON R., MILSON R.,

KITCHAN M., ELEVIN C., ST., PETER M., TREANARIS S., MILSON R.,

KITCHAN M., REFERIN S., ST., PETER M., TREANARIS S., MILSON R.,

KITCHAN M., REFERIN S., ST., PETER M., TREANARIS S., MILSON R.,

KITCHAN M., SERVIN S., ST., MAN M., MATERSTON R., MILSON R.,

KITCHAN M., SERVIN S., ST., MATERSTON R., MILSON R.,

KITCHAN M., SERVIN S., ST., MATERSTON R., MILSON R.,

KITCHAN M., SERVIN S., ST., MATERSTON R., MILSON R.,

KITCHAN M., SERVIN S., ST., MATERSTON R., MILSON R.,

KITCHAN M., SERVIN S., ST., MATERSTON S.,

KITCHAN M., SERVIN
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BULANYOTA, HETÄNADA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                      1-JAN-1988 (REL. 06, CREATED)
1-JAN-1988 (REL. 06, LAST EXQUENCE UPDATE)
1-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
200LYSIN SECRETION PROTEIN D, PLASHID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
UKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. FEBS-1995 (REL. 11. CREATED)
1. FEBS-1995 (REL. 11. LAST SEQUENCE UPDATE)
1. CCT-1996 (REL. 14. LAST ANNOTATION UPDATE)
TYOTHETICAL 51.1 KD PROTEIN IN DCD1-NRPL6 INTERGENIC RELIGH.
                            CEREICHA, COLI.
SEMID PHIVISI.
DEROBACTERIACERE.
TEROBACTERIACERE.
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ET_PHND: 2.

DAMPEDING SIGNAL.

25 DAMPEDING PROTEIN NEFA.

26 DAMPEDING PROTEIN NEFA.

27 DAMPEDING PROTEIN NEFA.

28 SIZE (POTENTAL).

29 SUCCEPT (POTENTAL).

29 LECCIDE 2 (POTENTAL).

30 LECCIDE 3 (POTENTAL).

30 LECCIDE 3 (POTENTAL).

31 LECCIDE 3 (POTENTAL).
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402
36257 MW; 3Flacaze cec32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 7; DB 1; Length 402;
Pred. No. 5.98e+00;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 7; DB 1; Length 465;
Pred. No. 5.98e+00;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYDROXYLATION (PROBABLE)
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                                                                                                                                                                                                                                                                                                                                                                                                 478 AA
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                RESULT 45

INCHINATION STANDARD; PRT; 478 AA. AC P0986;

D7 01-MAR-1989 (REL. 10, CREATED)
D7 01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
D7 01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
D7 01-COT-1986 (REL. 13, LAST METOFATION UPDATE)
D8 HENDLYSIN SECRETION PROTEIN D, CHROMOSONAL.
GN HITD.
GN HENDLYSIN SECRETION PROTEIN D, CHROMOSONAL.
GN HENDLYSIN SECRETION PROTEIN D, CHROMOSONAL.
GN HENDLYSIN GARLICUTES; SCOTOBACTERIA; FACULTAT
RESULTED FROM TABLE
RESULTED FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DE ARBIEDOLI STANDARD: PRT; 429 AA.
AC POSSI.
DY 01-AM-1988 (REL. 06, CREATED)
DY 01-AM-1988 (REL. 06, CAST SEQUENCE UPDATE)
DY 01-AM-1988 (REL. 06, CAST SEQUENCE UPDATE)
DY 01-CAM-1988 (REL. 06, CAST SEQUENCE UPDATE)
DY 01-CAM-1988 (REL. 06, CAST SEQUENCE UPDATE)
DY ARSENICAL PURP KEMBRANE PROTEIN.
OS ESCHERICHIA COLL.
OG PHANNID BY73.
CO EMPROBACTERIACHE.
HE 11 UPDATE PROM N.
HE 11 UPDATE PROM N.
HE 12 UPDATE PROM N.
HE 12 UPDATE PROM N.
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HE 14 UPDATE PROM N.
HE 15 UPDATE PROM N.
HE 15 UPDATE PROM N.
HE 15 UPDATE PROM N.
HE 16 UPDATE PROM N.
HE 17 UPDATE PROM N.
HE 18 UPDATE PROM NASERITE 
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Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%;
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671 KRAERLT 677
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1058 ISDTASL 1064
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MEDLINE: 92357011.
SCHUELEIN R., GENTSCHEV I., MOLLENKOPF H.-J., GOEBEL W.;
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HESS J., WELS W., VOGEL M., GOEBEL W.;
FENS MICROBIOL. LETT. 34:1-11(1986).
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ROKARYOTA; GRACILICUTES; SCOTOBACTERIA; PACULTATIVELY ANAEROBIC
NYTROBACTERIACEAE.
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Pred. No. 5.98e+00;
0; Mismatches 0; In
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0; Mismatches 0;
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Pred. No. 5.98e+00;
0; Mismatches 0; Indels
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AL HOL. GEN. GENET. 234:155-163(1992)

AL HOL. GEN. GENET. 234:155-163(1992)

CT. - SURCITION: INVOLVED IN THE TRANSPORT OF HEMOLITSIN A.

CT. - SURCITION: INVOLVED IN THE TRANSPORT OF HEMOLITSIN A.

CT. - STRICKLUTAR LOCATION: INVERSE MEMBRARE-BOUND (POTENTIAL).

ENG. HOLLS: GLOSSIS: TO THE HLTD PAMILY OF SECRETION PROTEINS.

ENG. HOLLS: GLOSSIS: TO THE HLTD PAMILY OF SECRETION PROTEINS.

PROS. HLTD PAMILY: INVERSE INVER MEMBRARE.

PROS. HLTD PAMILY: INVERSE MEMBRARE.

PROS. HLTD PA
Cuery Match 0.6%; Score 7; DB 1; Length 478; Best Local Similarity 100.0%; Pred. No. 5.98e+00; Smatches 0; Indela Matches 7; Conservative 0; Mismatches 0; Indela
                0
                Caps
                ö
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RESULT 46

IN OPRIJENZE STANDARD; PRT: 479 AA.
AC 051397; REL. 35, CREATED;
DT 01-NOV-1997 (REL. 35, LAST ESQUENCE UPDATE);
DT 01-NOV-1997 (REL. 35, LAST ESQUENCE UPDATE);
DT 01-NOV-1997 (REL. 35, LAST ANNOVATION UPDATE);
DE OUTER KEMBANET PROTEIN OPRIJECURSOR.
OR PROMARYOTA, GRACILICUTES; SCOTOBACTERIA; AEROBIC
PROMARYOTA, GRACILICUTES; SCOTOBACTERIA; AEROBIC
PROMARYOTA, GRACILICUTES; SCOTOBACTERIA; AEROBIC
PROTEITED (AND N. A.
RESULT PROTEITED (ULT-1996) TO ENGLICAERMANTO,DBM DATA BA
RESULT N. CHANGESHI J. NESHING COMPONENT OF A MULT
CC LEFULX PUNC.
CC 1-FUNCTION: CHANGEL-PONDING COMPONENT OF A MULT
CC 1-SIMILARITY BELONGS TO THE FUSA/MOUT FAMILY.
CC 1-SIMILARI

SEUDONONAS AERUGINOSA. VOKARYOTA, GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND PEUDONONADACEAE.

S (1)

P SEQUENCE PROM N.A.

C STRAIN-PAD;

C STRAIN-PAD;

A PROGLE K., GOTON N., TENJUNOTO N., ERAO Q., WADA A., TAMASAKI T.,

A RESHAT S., TAMAGISHI J., NISHIGO T.,

RESHAT S., TAMAGISHI J., NISHIGO T.,

AL SURMITED (ULL.1996) TO EMBLACERNANK, DIS JATA BANKS.

CC. I- FUNCTION: CHANNEL-PORNING COMPONENT OF A MULTIDROG RESISTANCE

CC. I- SINCLIAR LOCATION: ATTACHED TO THE OUTER MEMBRANE BY A LIPID CC.

CC. I- SINCLIAR TOTT. BELIANGS TO THE FUNLANDOT FAMILY.

DR PROSITE: PSOIDLIA, FROMAR_LIPOPROTEIN: 1.

DR PROSITE: PSOIDLIA, FROMAR_LIPOPROTEIN: LIPOPROTEIN: SIGNAL.

PROSITE: PSOIDLIA TOTTC RESISTANCE: LIPOPROTEIN: SIGNAL.

RE OUTER MEMBRANE: ANTHIBOTIC CRESTANCE: LIPOPROTEIN OPRJ.

FT CHAIN 20 479 AN: S1873 MY: ASTECONC CREST:

FT CHAIN 20 479 AN: S1873 MY: ASTECONC CREST:

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HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17). VIRIDAE: DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE; ALPHAHERPESVIRINAE

BEDUTHCE FROM N.A.

RECOURSE: 89.7 DALKITSPLE N.A., DAVISON N.J., DOLAN A., FRAME M.C.,

M. MCCENER: 89.7 DALKITSPLE N.A., DAVISON N.J., DOLAN A., FRAME M.C.,

M. MCCHAS D. PEREY L.J., SCOTT 1 B. TAILOR P.;

RL J. CEN VIROL. 69.1531-1574(1988)

CC ENT. 140. ERV-4 ULZJ. FACULT THAT CROUPS TOGETHER HSV-1 ULZJ.,

CC ENT. 140. ERV-4 ULZJ. AND VEV 18.

DR EMBL. 14112; E39321: -.

DR EMBL. 14112; E39321; -.

DR EMBL. 14112; E39321; -.

DR EMBL. 14112; E39321; -.

DR FIR; C30084 MMEM1. 57541 MW: 9CA25FA7 CRC32;

SO SEQUENCE 535 AA: 57541 MW: 9CA25FA7 CRC32;

Ouery Match 0.6%; Score 7; DB 1; Length 535; Best Local Similarity 100.0%; Pred. No. 5.98e+07; Matches 7; Conservative 0; Himatches 0; Indels

137 LRVRAGD 143 |||||| 717 LRVRAGD 723 0 Caps

TUZZI MSVIE STANDARD: PRT: 535 AA.
P09855:
O1-MAR-1999 (REL. 10, CREATED)
O1-MAR-1999 (REL. 10, LAST SEGUENCE UPDATE)
O1-DEC-1992 (REL. 24, LAST ANNOTATION UPDATE)
PROFEIN ULZI.

ridae; ds-dna enveloped viruses; herpesviridae; alphaherpesvirikae

SEQUENCE FROM N.A.
SEQUENCE 96.591165.
GOMPELS 0. MINSON A.):
GOMPEL

owery Match 0.6%; Score 7: DB 1; Length 535; Best Local Similarity 100.0%; Pred. No. 5.98e+07; Matches 7: Conservative 0; Mismatches 0; Indels .. Caps

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1998

Page 67

137 LRVRAQD 143 ||||||| 717 LRVRAQD 723

STEM_TEAST STADARD: PRT: 536 AA.

P48325: 008201:
01-FED-1996 (REL. 31, CREATED)
01-WOY-1997 (REL. 35, LAST REQUENCE UPDATE)
01-WOY-1997 (REL. 35, LAST ANNOTATION UPDATE)
CLITAMT:-FRN STRITETASE, HITOCHOMERAL (EC. 6.1.1.17) (GLITAMATE-TRNA
LICASE) (GLITS).

WELL OR TOLISH:
WELL OR TOLISH:
ENGLARION: CEMEVISIAE (BAREY'S FEAST).
ENARTOR: CHARANTASE ANNOTACTION: HEMILASCONICETES.

AGOLOFF A.A., SHTANKO A.; BMITTED (JAN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS RAIN-D273-10B;

Query Match 0.6%; Score 7; DB 1; Length 536; Best Local Similarity 100.0%; Pred. 80, 5.98e+00; Matches 7; Conservative 0; Mismatches 0; Indels Indels 0,

Gaps

59 LGSLRTA 65 |||||| 1115 LGSLRTA 1121

Search completed: Fri Dec 18 19:01:10 1998 Job time : 145 secs.

Page 65

Mon Dec 21 09:28:29 1998

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Page 66

Query Match 0.6%; Best Local Similarity 100.0%; Matches 7; Conservative Score 7; DB 1; Length 479; Pred. No. 5.98e+00; 0; Mismatches 0; Indels 0 Caps

9

292 AAEHRLR 298 ||||||| 553 AAEHRLR 559

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TZGL_MAGA STANDARD: PRT: 488 AA.
P43418;
01-MOV-1995 (REL. 12, CREATED)
01-MOV-1995 (REL. 13, LAST SEQUENCE UPDATE)
01-WOV-1995 (REL. 2), LAST SEQUENCE UPDATE)
01-WOV-1995 (REL. 2), LAST ANNOTATION UPDATE)
01-WOV-1995 (REL. 2), LAST ANNOTATION UPDATE)
1789 [11 RESTRICTION EMERINE SCAI (SC 3.1.21.4) (EMONUCLEASE RGAI)
(R. HGALL);

PROPHÍTUS CALLINARM. DEARTOTA: GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; STEDRELLACEAR.

TRAIN-HCTC 3438;

query Match 0.6%; Score 7; DB 1; Length 488; Best Local Similarity 100.0%; Pred. No. 5.98++00; Indels Matches 7; Conservative 0; Mismatches 0; Indels 0 Caps

0

Db 220 VPLLGSL 226 |||||| Qy 1112 VPLLGSL 1118

RESULT 48

ID 0121_HSV11

AC P10205;
DT 01-MAR-1989 (
DT 01-MAR-1989 (
DT 01-DEN 01992 (
DE PROTEIN UL21. (REL. 10, CREATED)
(REL. 10, LAST SEQUENCE UPDATE)
(REL. 24, LAST ANNOTATION UPDATE) STANDARD; PRT; 535 M

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866 6 0.5 1041 5 0.18011 NAD(7) TRANSPITDIOGENAS 6.91e-02 867 6 0.5 1031 4 005593 PRI-TERM CALCIDE-TRANSP 868 6 0.5 1031 4 005593 PRI-TERM CALCIDE-TRANSP 879 6 0.5 1062 1 005593 PRI-TERM CALCIDE-TRANSP 871 6 0.5 1062 1 005593 PRI-TERM CALCIDE-TRANSP 872 6 0.5 1072 1 055402 PRI-TERM CALCIDE-TRANSP 873 6 0.5 1072 1 055402 PRI-TERM CALCIDE-TRANSP 874 6 0.5 1072 1 055402 PRI-TERM CALCIDE-TRANSP 875 6 0.5 1112 1 055402 PRI-TERM CALCIDE-TRANSP 877 6 0.5 1112 1 055402 PRI-TERM CALCIDE-TRANSP 878 6 0.5 1112 1 055402 PRI-TERM CALCIDE-TRANSP 879 6 0.5 1112 1 055402 PRI-TERM CALCIDE-TRANSP 879 6 0.5 1114 1 055502 PRI-TERM CALCIDE-TRANSP 879 6 0.5 1114 1 055502 PRI-TERM CALCIDE-TRANSP 879 6 0.5 1114 1 055502 PRI-TERM CALCIDE-TRANSP 879 6 0.5 1116 2 051412 PRI-TERM CALCIDE-TRANSP 879 6 0.5 1116 2 051412 PRI-TERM CALCIDE-TRANSP 879 6 0.5 1116 2 051413 PRI-TERM PRI-TERM CALCIDE-TRANSP 879 6 0.5 1116 2 051413 PRI-TERM PRI-TERM CALCIDE-TRANSP 879 6 0.5 1116 2 051413 PRI-TERM PRI-TERM CALCIDE-TRANSP 879 6 0.5 1116 2 051413 PRI-TERM PRI-TERM CALCIDE-TRANSP 879 6 0.5 1116 2 051413 PRI-TERM PRI-TERM CALCIDE-TRANSP 879 6 0.5 1116 2 051413 PRI-TERM PRI-TERM CALCIDE-TRANSP 879 6 0.5 1116 2 051413 PRI-TERM PRI-TERM CALCIDE-TRANSP 879 6 0.5 1116 2 051413 PRI-TERM PRI-TERM CALCIDE-TRANSP 879 6 0.5 1116 2 051413 PRI-TERM PRI-TERM CALCIDE-TRANSP 879 6 0.5 1116 2 051413 PRI-TERM PRI-TERM CALCIDE-TRANSP 879 6 0.5 1126 1 0515413 PRI-TERM PRI-TERM CALCIDE-TRANSP 879 6 0.5 1126 1 0515413 PRI-TERM PRI-TERM CALCIDE-TRANSP 879 6 0.5 1126 1 0515413 PRI-TERM PRI-TERM CALCIDE-TRANSP 879 6 0.5 1126 1 0515413 PRI-TERM PRI-TERM PRI-TERM CALCIDE-TRANSP 879 6 0.5 1126 1 0515413 PRI-TERM PRI-TE	Mon Dec 21 09:28:30 1998 US-08-951-733-20.zept	764 6 0.5 770 5 0.18520 RPYENSE TRANSCRIPTAGE 6.91e-02 765 6 0.5 771 4 0.1450 RNOTELL GROWTH PACTOR BE 6.91e-02 766 6 0.5 772 1 0.08652 RNOTELL PRECORS 6.91e-02 767 6 0.5 772 1 0.08652 RNOTELL PRECORS 6.91e-02 768 6 0.5 772 1 0.08652 RNOTELL PRECORS 6.91e-02 769 6 0.5 772 1 0.08652 RNOTELL PRECORS 6.91e-02 770 6 0.5 774 1 0.02598 RNOTELL PRECORS 6.91e-02 771 6 0.5 774 1 0.02598 RNOTELL PRECORS 6.91e-02 772 6 0.5 774 1 0.02598 RNOTELL PRECORS 7.91e-02 773 6 0.5 775 1 0.03503 RNOTELL PROTEIN PACE 774 6 0.5 775 1 0.03503 RNOTELL PROTEIN PACE 775 6 0.5 775 1 0.03503 RNOTELL PROTEIN PACE 777 6 0.5 775 1 0.03503 RNOTELL PROTEIN PACE 778 6 0.5 776 1 0.03503 RNOTELL PROTEIN PACE 779 6 0.5 776 1 0.03503 RNOTELL PROTEIN PACE 779 6 0.5 776 1 0.03503 RNOTELL PROTEIN PACE 779 6 0.5 776 1 0.03503 RNOTELL PROTEIN PACE 779 6 0.5 776 1 0.03503 RNOTELL PROTEIN PACE 779 6 0.5 776 1 0.03503 RNOTELL PROTEIN PACE 779 6 0.5 776 1 0.03503 RNOTELL PROTEIN PACE 779 6 0.5 776 1 0.03503 RNOTELL PROTEIN PACE 779 6 0.5 776 1 0.03503 RNOTELL PROTEIN 779 6 0.5 776 1 0.03503 RNOTELL RNOTELL 779 6 0.5 776 1 0.03503 RNOTELL 779 6 0.5 776 1 0.03503 RNOTELL 770 770 770 770 770 770 770 770 770 770	Mon Dec 21 09:28:30 1998 US-08-951-733-20.rept
	Page 19		Page 17
917 6 0.5 1411 1 06122 COLLACEW ALPSA 1 TYPE 918 6 0.5 1441 4 015074 KLAMOSS PROTEST (FRAGERY) 920 6 0.5 1441 1 015075 KLAMOSS PROTEST (FRAGERY) 921 6 0.5 1411 1 015075 KLAMOSS PROTEST (FRAGERY) 922 6 0.5 1421 1 026525 REAL PROMESTS (FRAGERY) 923 6 0.5 1421 1 026525 REAL PROMESTS (FRAGERY) 924 6 0.5 1421 1 026525 REAL PROMESTS (FRAGERY) 925 6 0.5 1421 1 026525 REAL PROMESTS (FRAGERY) 926 6 0.5 1421 1 026525 REAL PROMESTS (FRAGERY) 927 6 0.5 1421 1 026525 REAL PROMESTS (FRAGERY) 928 6 0.5 1421 1 026525 REAL PROMESTS (FRAGERY) 929 920 921 922 923 924 925 925 926 927 927 928 928 929 929 929 929 929 929 929 929	Mon Dec 21 09:28:30 1998 U8-08-951-733-30.rept	815 6 0.5 818 13 091742 PIRROBLAST GROWTH PACT 6.91e-02 8176 6 0.5 812 4 011705 MANA (RIAMONS) POR OR 6.91e-02 8176 6 0.5 812 1 041186 MS SAMPA DOS DO PROTEIN 6.91e-02 8176 6 0.5 812 1 041186 MS SAMPA DOS DOS PROTEIN 6.91e-02 8176 6 0.5 812 1 041186 MS SAMPA DOS DOS PROTEIN 6.91e-02 8176 6 0.5 812 1 041186 MS SAMPA PROTEIN 6.91e-02 8176 6 0.5 812 1 041186 MS SAMPA PROTEIN 6.91e-02 8176 6 0.5 812 1 041186 MS SAMPA PROTEIN 6.91e-02 8176 6 0.5 812 1 041186 MS SAMPA PROTEIN 6.91e-02 8176 6 0.5 812 1 04184 MS SAMPA PROTEIN 6.91e-02 8176 6 0.5 818 1 05127 MS SAMPA PROTEIN 6.91e-02 8176 6 0.5 818 1 05127 MS SAMPA PROTEIN 6.91e-02 8176 6 0.5 818 1 05127 MS SAMPA PROTEIN 6.91e-02 8176 6 0.5 818 1 05127 MS SAMPA PROTEIN 6.91e-02 8176 6 0.5 817 1 05127 MS SAMPA PROTEIN 6.91e-02 8176 6 0.5 817 1 05127 MS SAMPA PROTEIN 6.91e-02 8176 6 0.5 817 1 05127 MS SAMPA PROTEIN 6.91e-02 8176 6 0.5 817 1 05127 MS SAMPA PROTEIN 6.91e-02 8176 6 0.5 817 1 05127 MS SAMPA PROTEIN 6.91e-02 8176 6 0.5 817 1 05127 MS SAMPA PROTEIN 6.91e-02 8176 6 0.5 817 1 05127 MS SAMPA PROTEIN 6.91e-02 8176 6 0.5 817 1 05127 MS SAMPA PROTEIN 6.91e-02 8176 6 0.5 817 1 05127 MS SAMPA PROTEIN 6.91e-02 8176 6 0.5 817 1 05127 MS SAMPA PROTEIN 6.91e-02 8176 6 0.5 81	Mon Dec 21 09:28:30 1998 US-08-951-733-20.zept

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	Page 23		Page 21
RX MEDILINE, 97431088. RA CADDIES D. A. COUNTRE C.M. BAIJESBERGEN R.L., DAVIDOFF N.J., LIU O., RA CADDIES D. A., WRIBBERGEN R.L., DAVIDOFF N.J., LIU O., RA CADDIES D. A., WRIBBERGEN R.L., DAVIDOFF N.J., LIU O., RA CADDIES D. A., WRIBBERGEN R.L., DAVIDOFF N.J., LIU O., RA CADDIES D. A., WRIBBERGEN R.L., DAVIDOFF N.J., LIU O., RACCERTIES, CASACISTIS. DE ENEL, APOSINIS, CASACIS. DE CADOLINA DE CONTRE DE CASACILLES DE C	Mon Dec 21 09:28:30 1998 US-08-951-733-20.zept	RX MEDIAS, T.M., MORIN G.B., CIDAPMAN R.B., WEINSTER S.L., ANDREWS W.H., RAMADIA, T.M., MORIN G.B., CENDRAN R.B., WEINSTER S.L., ANDREWS W.H., RAMADIA, T.M., MORIN G.B., CENDRAN R.B., WEINSTER S.L., ANDREWS W.H., RAMADIA, T.M., MORIN G.B., CERNICA, C.B., CERNICA, C.B., C.B	Mon Dec 21 09:28:30 1998 US-08-951-733-20.zapt

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Page 26

SUBMITTED (OCT-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL, APO29335; G2805903; .
NOW_TER 51 57
NOW_TER 67 67

Query Match 1.9%; Best Local Similarity 100.0%; Matches 22; Conservative

Score 22; DB 11; Length 67; Pred. No. 3.99e-42; 0; Mismatches 0; Indels 0;

Gaps

0

NON_TER 67 67 SEQUENCE 67 AA: 8368 MW;

E2A06F2B CRC32;

1081 KIRRHVTYPLIGSLETAQTQLSRKLPGTTLALALANALPSDFKTILD 1132 1103 KIRRHVTYPLIGSLETAQTQLSRKLPGTTLALLALALIHIHIHIHIHIHI 1103 KIRRHVTYPLIGSLETAQTQLSRKLPGTTLALLALANALPALPSDFTTILD 1154 1001 PROQUMENTPEPELEVISDENSICYSILKAKNACHSICAKCAACDELBERVOMICHQAETI. 1080 961 NRGFRAGRUREKLEVLELKCHSLEFIDLOVESLOFVCHYTKILLLANTERBUCHGLE 1020 983 NRGFRAGRUKEKLEVLELKCHSLEFIDLOVESLOFVCHYTKILLLANTERBUCHGLE 1042 901 RETVYNFPVEDEALGGENFYGNFANGLFMCGLLLDTRELEVGSDYSSYNTGENSLETP 900 RETVYNFPVEDEALGGENFYGNFANGLFMCGLLLDTRELEVGSDYSSYNTGENSLETP 902 921 RETVYNFPVEDEALGGENFYGNFANGLFMCGLLLDTRELEVGSDYSSYARTSENSLETF 902 661 LFSVLWTERARROLLOASVIGLODIBANRFYLWAWAQDPPELYFYKVYYTGAVIT 720 683 LFSVLWTERARROCLOASVIGLDDIBANRFYLWWAQDPPELYFYKVYYTGAVIT 742 601 LSELETWOHRELRALLITSRLEF PKPDGLRF IVADDYVGARTFRREKANERLISRVEA 613 LSELETWOHRELRALLITSRLEF PKPDGLRF IVADDYVGARTFRREKANERLISRVEA 613 LSELETWOHRELRAPALLITSRLEF PKPDGLRF IVADDYVGARTFRREKANERLISRVEA 660

RESULT:

1 DP STATE A SPECIALINARY; PRT; 1122 AA.

2 O70372; PRELIMINARY; PRT; 1122 AA.

2 PRELIMINARY; PROBLEME. 07, LAST ANNOTATION UPDATE)

2 PRELIMINARY; PROBLEME. 07, LAST ANNOTATION UPDATE)

3 MUS MOSCULUS (NODES).

3 MUS MOSCULUS (NODES).

4 PRELIMINARY; PROM N.A.

4 CHECKENERGE RA., ALEGOPP R.C., CHIN L., MORIN G.B., DEPINHO R.A.;

5 PROLIMINARY; CHIN PRELIMINARY;

5 PROLIMINARY; CHIN PRELIMINARY;

5 PROLIMINARY;

5 PROLIMINAR

Query Match 1.94; Score 22; DB 11; Length 1122; Best Local Similarity 100,04; Prac4 No. 199-42; Matches 22; Conservative 0; Mismatches 0; Indels

Caps 0

SECURNCE FROM N.A., ALLSOPP R.C., CHIN L., MORIN G.B., DEPINHO R.A.:
GREENBERG R.A., ALLSOPP R.C., CHIN L., MORIN G.B., DEPINHO R.A.:
ONCOCERN 0:0-0(1599)
EMBL: RAPOSIBLE:
GROUNGE: 1122 AA: 127977 MM; 222075D6 CRC32;

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RESULT

ID 035432 PRELIMINARY: PRT: 67 AA.

C 035432 PRELIMINARY: PRT: 67 AA.

C 035432 PRELIMINARY: PRT: 67 AA.

C 035432 PRESIDENT. 05, CREATED)

OT 01-ANN-1998 (TREMBLERT. 07, LAST ANNOTATION UPDATE)

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EQUIRNO FROM N.A.
MEZHANE, 809656.
SAGA Y.E., TUNG-656.
SAGA Y.E., TUNG-656.
HOL. CELL. BLOL. 8 4489-4895(1988).
PERMI: MAJ354: G5541921 - 4895(1988).
TRANSMEMBANE. ALTERNATIVE SPLICING: TRANSMEMBRANE.
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NOLTER EUKARYOTA; METAZOA; CHORDATA; EUTHERIA; RODENTIA.

83222222222000

Query Match 0.8%; Best Local Similarity 100.0%; Matches 9; Conservative Score 9: DB 11; Length 24; Pred. No. 9.84e-04; 0; Mismatches 0; Indels 0 Gaps 0

10 LAFGFALLD 18 |||||||| 119 LAFGFALLD 127

RESULT 6

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RESULT 6

RESULT 6

RESULT 1814 PRELIMINAT: PRT: 183 AA.

AC 0.884: PRELIMINATION OFFATE)

DT 01-80V-1986 (TREMBLEM: 0.1.487 EMUTRICON OFFATE)

DE LY-5 GLYCOPPOTEIN PREDUNEON (PRAGMENT).

CO ENTANYOTA, METANON, CHONDATA, VERTEBRATA, TETRAPODA, MAMAALIA;

RE 11

RE 500MENTE 187460997.

RA SAAA T. TUNG J. S. SHEN F.W. BOYSE E.A.:

PROC. MATH. MACAD. SCI. U.S.A. 84:5384-5388(1987).

RE 250MLNE, 187320, 6321198;
PR 510ML, MALTERNATIVE SPLICING.

RE 510ML, MALTERNATIVE SPLICING.

PT 510ML, MALTERNATIVE SPLICING.

PT 184 A. SAAA T. 178 J. S. SHEN F.W. BOYSE E.A.:

PT 510ML, MALTERNATIVE SPLICING.

PT 510ML, MALTERNATIVE SPLICING.

PT 184 A. SAAA T. 178 J. SAA: 18601 MH; 37DE42ED CRC32:

SEGUENCE PROM N.A.

SEGUENCE PROM N.A.

SEGUENCE PROM N.A.

SEGUENCE PROM J.S. SHEM P.W. BOTGE E.A.;

SEGUENCE NATI. ACAD. SCI. U.S.A. 845364-5368(1987).

BERL: N1720; G621399;

SEGUENCE NATIONAL SECUENCE SEGUENCE 183 AA; 18601 MH; 37DE42ED CRC32;

문 Ouery Match 0.8%; Score 9; DB 11; Length 183; Best Local Similarity 100.0%; Pred. No. 9.84-04; Matches 9; Conservative 0; Hismatches 0; Indels 8 LAPGFALLD 16 |||||||| 119 LAPGFALLD 127 0 Gaps

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Page 27

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TRESULT 5
PRELIMINARY; PRT: 24 AA.

1D 061915
PRELIMINARY; PRT: 24 AA.

1D 01915
PR 01 NOV-1996 (TREMBLEEL 01, CREATED)
PR 01 NOV-1996 (TREMBLEEL 01, LAST REQUENCE UPDATE)
PR 10 NOV-1996 (TREMBLEEL 01, LAST REQUENCE UPDATE)
PR 10 NOV-1996 (TREMBLEEL 01, LAST REWORTION UPDATE)
PR 10 NOV-1996 (TREMBLEEL 01, LAST REWORTION UPDATE)
PR 10 NOV-1996 (TREMBLEEL 01, LAST REWORTION UPDATE)

MUS MUSCULUS (MOUSE).

Page 28

RESULT 7
10 01493 PRELIMINARY PRT: 632 AA.
AC 01492 PRAN-1998 (PREMBLEEL OF LAST ENURYNTION UPDATE)
DE ADS COMPLETE CINS.
BHOM SANIERS (ENDAM).
CE ETHANTON, MITANON, CHORDATA; VERTEBRATA; TETRAPODA; MAMALIA;
RN 12012NCE FROM N.A.
RN SEQUENCE FROM N.A.
RN TORICHTHE, STATONO,
RN YORKINGH, A. SOUNTR R. MASUNARA M., KONITA S., INOUE A.,
RN TORICHTHE, A. POUCHER PROMISSION, DATES
ETHAL SHOOLOGO; DATES
SEQUENCE 632 AA: 61727 MH; ABADBORD CRC32; Query Match

Best Local Similarity 100.0%;
Matches 9; Conservative 515 VRAQDPPPE 523 |||||||| 719 VRAQDPPPE 727 Score 9; DB 4; Length 632; Pred. No. 9.84e-04; 0; Mismatches 0; Indels 0 Caps

SEQUENCE PROM N.A.
STRAIMS-972H:;
KEDLINE: 97400631,
MANAMEA T.M., MORAIN G.B., CHAPMAN K.B., WEINRICH S.L., ANDREWS W.H.,
LINGERE J., HALEF C.B., CECH T.R.;
GCIENCE 277:955-959(1997). SEGUENCE FROM N.A. STRAIN=972H-; LYNE M., RAVANDREAM M.A., BARRELL B.G., VOLCKAERT G.; 01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAGC-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
TELOMERASE REVERSE TRANSCRIPTASE 1. SCHIZOSACCHAROMYCES POMBE (FISSION YEAST). PRELIMINARY; PRT; 988 AA

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TRESULT 12

ID 065210, PRELIMINARY; PRT; 146 AA.

AC 065210, 05210, 075249LHEL. 01, CREATED)

DT 01-NOV-1996 (TREMBLEEL 01, LAST SEQUENCE UPDATE)
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AC 061812;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
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                                                                                                                                                                                     Query Match 0.8%;
Best Local Similarity 100.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Owery Match 0.8%; Score 9; DB 3; Length 989;
Best Local Similarity 100 0%; Pred. No. 9.84e-04;
Matches 9; Conservative 0; Mismatches 0; Indels
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SECUENCE 1343 AA: 150679 MW; 984DFAEB CRC32;
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NAKANDAN TM., MORIN G.B., CHAPMAN K.B., WEIRRICH S.L., ANDREWS H.B., LIKHGHER J., HARLET C.B., CECH T.R.;
SCIENCE 277-955-7595(1997).

EMGL. RADIS-783, G2340168; ...
FRAM, PRODUS-781, FT.
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119 LAFGFALLD 127
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                                                                                                                                                                                     Score 9: DB 11; Length 1343;
Pred. No. 9.84e-04;
0; Mismatches 0; Indels 0;
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ID 064730

OC 064730

OT 01-NOV-1996 (TREMEMEEL 01 CREATED)

DT 01-NOV-1996 (TREMEMEEL 01 LAST SEQUENCE UPDATE)

DT 01-NOV-1996 (TREMEMEEL 01 LAST SEQUENCE UPDATE)

DT 01-NOV-1996 (TREMEMEEL 01 LAST SEQUENCE UPDATE)

DE LEUCCCTTE COMMON ANTIGNN (L-CA) (FRAGMENT)

OS HUS MUSCULUS (MOUSE)

OC EUTHARTOTA METAKOA: CHORDATA; VERTERRATA: TETRAPODA; MAMMALIA;

RN 11

RP SEQUENCE OF 1-1256 FROM H.A.

RX MEDILINE: 87260986.

RA TIROMS M.L., REFNOLUS P.J., CHAIN A., BEN-NERIAH Y., TROMERIDGE I.:

RN 12

RN 17811. ACAD. SCI. U.S.A. 84:5380-5363(1887).

RN 17812. SCI. U.S.A. 84:5380-5363(1887).

RN 17813. SCI. SCI. U.S.A. 91:6EL J.T., TROMAS M.L.;

RN 17813. SCI. CHEM. AG4:6210-6219(1898).
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     Dec 21 09:28:30
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Best Local Similarity 100.0%;
Matches 9; Conservative
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DEW. COMP. IMMUNIC. 1:443-254(1991).
EMEL. M92393; G19891).
HOD; MGI:97310; PPPRC.
PROSITE: P80043; TTL PHOSPHATASE_1; 2.
PFMA: PF00041; ft.3.
PFMA: PF00041: T_phosphatase.
SIGNAL: HTDROLASE.
SIGNAL: HTDROLASE.
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CHAIN 24 1291 LYMPHOCTIE COMMON ANTIGEN.
SEQUENCE 1291 AA; 144559 MW; 63481A8D CRC32;
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01-UNF-1996 (TREMELREL, 05. LAST SECRECE UPDATE)
PROTEIN TROSHE PROSPIATASE, RECEPTOR TYPE, C PRECURSOR (EC 3.1.3.48)
(LIMPRICETE COMBON ANTICEN)
PEPERC OR LYS.
HIS NECCULS (MOUSE)
HIS NECCULS (MOUSE)
HIS NECCULS (MOUSE)
SEQUENCE FROM N.A.
STRAIN=BA71V;
MEDLINE; 93346971.
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRALM=BA71V;
MEDLINE; 91134988.
CAMACHO A., VINUELA E.;
VIROLOGY 181:251-257(1991).
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAINBANIV;
KEDLINE; 90219204.
ALMENDRAL J.M., ALMAZAN F., BI
ALMENDRAL J.M., ALMAZAN F., BI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-BANIV.
MEDLINE, 90219205.
CONEALER A., CALVO V., ALMARAN F
LA VEGA I., BLASCO R., VINUELA E
J. VIROL. 64:2073-2081(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUC-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
PDP146L.
DP146L.
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STRAIN-BATIN;
TAMEE R.J., RODRIGUEZ J.M., P
RODRIGUEZ J.F., VINUELA E.;
TANDECICT 208:249-278(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 LAPGFALLD 16
| | | | | | | | |
| 119 LAPGFALLD 127
                                                               SEQUENCE FROM N.A.
STRAIN-BA71V;
A VEGA I., GONZALE
                                                                                                                                                                                                                       RAIN-BA71V;
                                                                                                                                                                                     MAZAN F., MURGUIA J.R.,
GEN. VIROL. 0:0-0(0).
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RIDAE: DS-DNA NONENVELOPED VIRUSES;
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ROLOGY 201:152-156(1994).
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Pred. No. 9:84e-04;
0; Mismatches 0: Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F., ALMENDRAL J.M., RAMIREZ J.C., E.;
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                                                                                                                                                                                                        LA VEGA
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Best Local Similarity 100.0%;
Matches 8; Conservative
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SULT 1
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STRAIN-BA71V;
MEDLINE; 92087485.
RODRIGUEZ J.M. SALAS M.L., V
VIROLOCY 186:40-52(1992).
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SEQUENCE FROM N.A.
STRAIR-BATIV;
MEDLINE; 94085774.
YANEE R.J., RODRIGGEZ J.M., E
GENE 134:161-174(1993).
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142 RSYLPNTV 149
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    SENDURNEE FROM N.A.
STRAIN-COOPER,
KIADA A., TIKOO S.K., BABIUK L.A., HURK S.;
GENE 0.0-0(0).
ENGL; 014-93; G114326; ...
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EMBL: U18466; G780518; -.
SEQUENCE 146 AA; 17258 MN; 82574504 CRC32;
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SERALMER 8016328
GONALEZ A., TALAVERA A., ALMENDRAL J.M., VINUZIA E.;
NUCLEIC ACIIS RES. 14:6835-6844(1986).
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STRAINHEATUY.
REDLINE: 94123986.
RODRIGUEZ J.H., YANEZ R.J., RODRIGUEZ J.P.,
GENE 136:103-110(1993).
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STRAIN-BAIV,
RODRIGUEZ JA. YANEE R.J., ALMEAN P.,
J.VIROL. 67:5313-5330(1993).
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BERLINE: 92277388
MUNCE M., PERLE J.M., SALAS M.L., VINUELA E., LOPEZ-OTIN G.;
ANCH. VIROL. 130:93-107(1993).
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70, CEN. VIROL. 74:1633-1638(1993).
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STRAIN-BA71V;
YANEZ R.J.;
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STRAIN-BATVI;
NEDLINE: 95018315.
NEDLINE: 95018315.
LICANA C., EIRAS A., YANEZ R.J.,
LADANSO C., RODDICOTER J. F., ESCRIBANO J.M.;
J. YIROL. 68:7244-7252(1994).
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STRAIN-BAIV:
MEDLINE; 90213993.
LOPEZ-OTIN C., FREIJE J.M., PARRA
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STRAIMERATIVE
REDILTER, 93281390.
TANEER R.J.: BOUGSTELL M., NOCAL M.L., TUSTE L., VINUELA E.;
PUCLEIC ACIDS RES. 31:3433-3437(1993).
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STRAIN-BA71V;
MEDLINE; 90357780.
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STRAIN-BA71V;
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LLCAMI A., ANGULO A., VINUELA E.;
J. GEN. VIROL. 74:2317-2324(1993)
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ASCO R., LOPEZ-OTIN C., MUNOZ M., BOCKAMP E.O., SIMON-MATEO C.,
KNUELA E.;
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                                                                                                                                                                                                                                                                                                      CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 1.57e-01;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                   HERPESVIRIDAE; ALPHAHERPESVIRINAE
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ID 083745; PRELIMINARY, PRT; 342 AA.

AC 083745; PREDELREL 01, CREATED)

DT 01-NOV-1996 (TREMELREL 01, LAST SEQUENCE UPDATE)

DT 01-NOV-1996 (TREMELREL 01, LAST SEQUENCE UPDATE)

PROVIDAL V-905.

OS MYZUPOROLIFERANTIC SARCOMA VIRUS.

OC VIRILAE, SS-RMA ENVELOPED VIRUS.

RE 110

RE SEQUENCE FROM N.A.

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RE SEQUENCE FROM N.A.

RE SEQUENCE FROM N.A.

RE SEQUENCE TROM N.A.

RE SEQUENCE N. AMBUTTANTIC C. ROLLEK R., COGGINS L., OSTERTAG W.;

RE STACET A. RAMBUTTANTIC SARCOMA SECUENCE N. OSTERTAG W.;

RE SEQUENCE N. AMBUTTANTIC SARCOMA SECUENCE N. OSTERTAG W.;

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RE PEMB. TROPOSEN SECUENCE N. SARCOMA SECUENCE N. 
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RESULT 15

ID 011254, PRELIMINARY; PRT; 500 AA.

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Best Local Similarity 100.0%;
Matches 8; Conservative
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SEQUENCE FROM N.A.
SETALHHANIV;
MEDILHE, 9515942B
SINON-MATED C., PERLIE J.M., ANDRES G.
VINOLOGI 206:1140-1144(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-BA71V;
MEDILINE: 93174976.
YANEE R.J., VIRUELA E.;
VIRCLOGY 193:531-536(1993).
                                                                                                                                                                                                                                                                                                                                                                                             291 LRPSLTGA 298
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372 LRPSLTGA 379
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243 ARRRGGSA 250
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STRAIN=BATIV;
KEDILNE: 94091056.
FREXITE J.M., LAIN S., VINUELA E.,
VIRUS RES. 30:63-72(1993).
[25]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAINS-MOTIVE
MEDINE: 92163807
GARCIA-BEATO R., FREIJE J.M., LOPEZ.
SAANS M.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŚEQÓZNCE FROM N.A.
STRAINBANIV;
KEDLINE; 93174941.
PERN L., TANEZ R.J., REVILLA Y.,
PUROLOGY 193:319-328(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŚEDŪZNCE PROM N.A.
STRAIN=8A71Y;
KEDLINE; 9333310.
PRADOS F.J., VINUELA E., ALCAMI A.;
PRADOS F.J., VINUELA E., ALCAMI A.;
J. VIROL. 67:2475-2485(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [17]
SEQUENCE FROM N.A.
STRAIN-BA71VY
STRAIN-BA71VY
STRAIN-BA71VY
STRAIN-BA71VY
SEDON-NATED C., ANDRES G., VINUELA E.;
DEMON J. 12:2977-2987(1993).
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TRAINBAIN;
REDLINE; 92360660.
LICAMI A., ANGULO A., LOPEZ-OTIN C.,
ARRAGEOSA A.L., VINTELA E.;
TVIROL. 66:3860-3868(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ROLOGY 188:938-947(1992).
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Pred. No. 1.57e-01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 8; DB 14; Length 338;
Pred. No. 1.57e-01;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOPEZ-OTIN C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOPEE-OTIN C., VINUELA E.
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36

Dec 21 09:28:30 1998

Page 33

Dec 21 09:28:30

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US-08-951-733-20.rspt

Page 37

Mon Dec 21 09:28:30 1998

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P SEQUENCE FROM N.A.

C TISSUE-ADRESMA, CLAND;

X HEDLINE; 97208876.

A ROWERA C., MANDAYASSII C., NISHIMORI K., MIZUNO S.;

L GENE 185:217-222(1997).

C 1- SINILARIT: BELOWS TO THE CITOCHROME P450 FAMILY.

R EMBL. P45013; G13087711.

R PROSITE: P800081; CTCOCHROME_P450; 1.

R PROSITE: P800081; P550-CXTGENASE, ELECTRO TRANSPORT; HEMBANNE; HEM

R STRUMBURG 1850 AN: 58195 NP: 88384C4F CRC12;

C SEQUENCE 508 AN: 58195 NP: 88384C4F CRC12;

HE

5 Query Match 0.7%; Score 8: DB 13; Length 508; Best Local Similarity 100.0%; Pred. No. 1.57e-01; Matches 0; Indels Matches 0; Indels 0 Gaps

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430 SRSLPLPK 437 |||||||| |251 SRSLPLPK 258

Query Match 0.7%; Best Local Similarity 100.0%; Matches 8; Conservative

Score 8; DB 5; Length 869; Pred. No. 1.57e-01; 0; Mismatches 0; Indels

<u>.</u>,

Gaps 0

128 PYGVLLKT 135 |||||||| 426 PYGVLLKT 433 PRT;

CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE) 680 AA

DICTYOSTELIUM DISCOIDEUM (SLINE MOLD). EURANYOTA, PROTOZOA, SARCOMASTIGOPRORA; SARCODINA; RHIZOPODA; EUNYCETOZOA; DICTYOSTELIA.

SEQUENCE 680 AA; 76448 MW; 28EBB680 CRC32; LOOMIS W.F., IRANFAR N.;
SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA
EMBL, AF019982; G2425115; -.

Overy Match 0.7%; Score 8; DB 5; Length 680; Best Local Similarity 100.0%; Pred. No. 1.57e-01; Matches 8; Conservative 0; Mismatches 0; Indels 0 Caps

9

LEA MAUS (HAIE). EURANYON, PLANYA, EMBRYOPHYTA; ANGIOSPERMAE; NONOCOTYLEDONEAE: CYPERALES; GRAMINEAE.

CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)

PRT; 106

SECURNCE FROM N.A.

GTRAINSON

KEDLINE: 9335569.

BECRAFT P. N. STINAED P. S., MCCARTY D.R.;

BECRAFT P. N., STINAED P. S., MCCARTY D.R.;

BEDL. U6427; GL59739.

BEDL. U6427; GL59739.

R PRAN. PRODOGO. THRE.G.

R PRAN. PRODOGO

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US-08-951-733-20.rspt

Page 39

Mon Dec 21 09:28:30 1998

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Page 40

Query Match 0.7%; Best Local Similarity 100.0%; Matches 8; Conservative

ISSUE-BRAIN;

TANAKA A., KOTANI H.,

NOMURA N.,

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941 ALAPATPA 948 |||||||| 15 ALAPATPA 22

RESULT 10

RESULT 10

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1998

83 CGLLLDTR 90 |||||||| 953 CGLLLDTR 960

127 19
060300 PRELIMINARY; PRT; 1095 AA.
060300; 070300 PREMIMENT; PRT; 1095 AA.
060300; 071-NGC-1988 (TREMGLEEL. 07; CREATED)
01-NGC-1988 (TREMGLEEL. 07; LAST SEQUENCE UPDATE)
01-NGC-1988 (TREMGLEEL. 07; LAST SEQUENCE UPDATE)
01-NGC-1988 (TREMGLEEL)
01-NGC-1988 (TREMGL

AGASE 1. ISHIKAWA K., MIYAJIMA N., HARA O.; NA RES. 5:31-39(1998). WEL, ABOILI25; D1026409; -.

SEQUENCE 1095 AA; 118835 MW; 43474254 CRC32;

Query Match
Best Local Similarity 100.0%;
Matches 8; Conservative Score 8: DB 4: Length 1095; Pred. No. 1.57e-01; 0; Mismatches 0; Indels

Score 8; DB 10; Length 901; Pred. No. 1.57e-01; 0; Mismatches 0; Indels 0;

Gaps

0

SEQUENCE PROM N.A.

STRAIN=04-2;

NEDLINE; 95119139.

MADEDDU L., GAUTIER M.C., LE
BIOCHIMIE 76:329-335(1994).

LE CAER J.P.,

DE LOUBRESSE N., SPERLING L.;

STOCHECE FROM N.A.
STRAINFOA-2;
MIDDLINE, 96058477.
MADEDDU L. GANTIER H.C., VAYSSIE L., HOUARI A., SPERLING L.;
MADEDU L. CELL 6:693-659(1995).
EMBL UJ7510, 6881410;
MARRIX PROTEIN.
10M.TER
13 1 21
880ERECE 13 AA; 2706 MH; AB72C0F4 CRC12;

Query Match 0.6%; Best Local Similarity 100.0%; Matches 7; Conservative Score 7; DB 5; Length 23; Pred. No. 1.47e+01; 0; Mismatches 0; Indels Gaps

7 VSTLTDL 13 ||||||| 785 VSTLTDL 791

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RESULTS 21

120 OF5812 PRELIMINARY PRT: 37 AA.
AC 05813 PRELIMINARY PRT: 37 AA.
AC 05813 PRELIMINARY PRT: 30 AA.
AC 05813 PRELIMINARY PRANCIENT OF DATE PROPRETION PROPRETION PROPRETION PRANCIS PRANCIS PRANCIS PRANCIS PRANCIS PRANCIS PRANCIS PRANCIS PROPRETION A.
AC 05813 PRELIMINARY PROPRETION PROPRIST OF DASIL/GENEARY/DDSJ DATA BANKS.
BY 0504000 PROPRIST PROPRETION PROPR

NON_TER 1 1 NON_TER 37 37 37 SEQUENCE 37 AA; 4205 MW; 507621E0 CRC32;

owary Match 0.6%; Score 7; DB 10; Length 37; Best Local Similarity 100.0%; Pred. No. 1.47+c01; Matches 7; Conservative 0; Mismatches 0; Indels

Indels 0

Gaps

0

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PESCUTA 17

ID 024144

PRELIMINARY; PRT; 869 AA.

AC 024144

DT 01-NOV-1996 (TREMELEEL, 01, CREATED)

DT 01-NOV-1996 (TREMELEEL, 01, LAST SEQUENCE UPDATE)

DT 01-NAV-1996 (TREMELEEL, 01, LAST SEQUENCE UPDATE)

DT 01-NAV-1996 (TREMELEEL, 02, LAST ANNOTATION UPDATE)

DE HATURNED PROTEIN.

GN 1H

OS DROSOPHILA MELANGCASTER (PRUIT FLY).

CC EUTARCTOR; METAGACA: ARTHROPODA; INSECTA: DIFTERA.

RN 1212ETCH; EFFOCM N.A.

RN SEQUENCE PROM N.A.

RN SEQUENCE PROM N.A.

RN DEPLEMENT 11 021550 161.

DR TLYANGE, PSOC 1965 1.3

SQ SEQUENCE 869 AA: 97969 MM; E395B888 CRC12;

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RESULT 26

OR OSCIPPION PRELIMINARY: PRT: 117 AA.

TO COSCIPPION (TREMGLEREL. 01, CREATED)

TO 1-MVV-1996 (TREMGLEREL. 01, LAST SCOURME UPDATE)

TO 1-MVV-1996 (TREMGLEREL. 01, LAST SCOURME UPDATE)

TO 1-MVV-1996 (TREMGLEREL. 01, LAST ANNOTATION UPDATE)

TO 1-MVV-1996 (TREMGLEREL. 01, LAST ANNOTATION UPDATE)

TO 1-MVV-1996 (TREMGLEREL. 01, LAST ANNOTATION UPDATE)

TO 1-MVV-1996 (TREMGLEREL. 02, LAST ANNOTATION UPDATE)

TO 1-MVV-1996 (TREMGLEREL. 03, LAST ANNOTATION UPDATE)

TO 1-MVV-1996 (TREMGLEREL. 01, LAST ANNOTATION UPDATE)

TO 1-MVV-1996 (TREMGLEREL 01, LAST ANNOTATION UPDATE)

TO 1-MV
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10 AA.

10 31809.

DT 01-NOV-1996 (FREMELREL 01, CREATED)
DT 01-NOV-1996 (FREMELREL 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (FREMELREL 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (FREMELREL 01, LAST SEQUENCE UPDATE)
DE RHPA (FRAMENT).
DE STRETPOCOCCUS CRISTA.

OG PHASHID PSCHAOO2.
OC PHOKARTOYA, BACTERIA; FIRMICUTES; GRAM-POSITIVE COCCI;
OC STRETPOCOCCACEAE.
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-CCSA;
RA CORREIA F.F., DIRIENZO J.M., NCKAY T.L., ROSAN B.;
RH CORREIA F.F., DIRIENZO J.M., NCKAY T.L., ROSAN B.;
RH CORREIA F.F., GRAM-POSITIVE COCCI;
RN 118PET. THOMM. 64: 32114-2121(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REAL STREET STREET STREET
           RESULT 27
ID 073311
AC 073311;
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Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%; Pred. No. 1.47e+0;
Matches 7; Conservative 0; Mismatches 0; Indels
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STRAIN-2 A.I.

STRAIN-2 A.I.

MEDILNE: 9005223 H., KAPLAN S.;

A EMILSTRA. REVALES J.H., KAPLAN S.;

J. BACTERIOU. 177.6422-6431(1995).

R EMBL. 035443; G1072669;

T NON TER

113 113

SEQUENCE 113 AA: 11864 MF; 08A79AA1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.6%;
Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                    65 ARRRGGS 71
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243 ARRRGGS 249
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152 ALRGSGA 158
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|||||||
183 LVAPSCA 189
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SEQUENCE 87 AA; 9613 MW; 3DE25EOA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     052175 PRELIMINARY: PRT: 07 A.
052175 PRELIMINARY: PRT: 07 A.
01-JUN-1998 (TREMBLEEL. 06, CREATED)
01-JUN-1998 (TREMBLEEL. 07, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLEEL. 07, LAST SEQUENCE. UPDATE)
PLASHID PERT, COMPLETE PLASHID SEQUENCE.
SALMONELLA BERTA.
PROMANION: GRACILICUTES; SCONDACTERIA: FACULTATIVE
PROMANION: GRACILICUTES; SCONDACTERIA: FACULTATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 RPSFLLS 11
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364 RPSFLLS 370
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HANES D.E., KEASLER S.P., LAMPEL K.A.;

SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS

EMBL. P025795; G2689636; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
ROBISON K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TEROBACTERIACEAE
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                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                      Score 7; DB 2; Length 117;
Pred. No. 1.47e+01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 7; DB 2; Length 87;
Pred. No. 1.47e+01;
0; Mismatches 0; Indels 0;
                                             PRT;
                                             125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-951-733-20.rspt
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RESULT 28

ID 05591:
D 05591:
D 05591:
DT 01-NOV-1996 (TRENDILEEL. 01. CREATED)
DT 01-NOV-1996 (TRENDILEEL. 01. LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TRENDILEEL. 01. LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TRENDILEEL. 01. LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 14.4 KD PROTEIN.
OS SYNECHCUSTIS SP.
OC CHROCOCCALES.
OC CHROCOCCALES.
RN [1]
RP SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
NEED OT. TANABAA N., SATO S., KOTANI H., SAZUKA T., KI
DAN ARSE. J. 153-156(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 24

RESULT 24

RESULT 24

AD 0293, PRELIMINAT: PRT: 111 AA.

AD 0293, PRELIMINAT: PRT: 111 AA.

AD 0293, PRELIMINAT: OLICARITED

DT 01-NNV-1996 (TREMBLEEL. 01, LAST REFORENCE UPDATE)

DT 01-NNV-1996 (TREMBLEEL. 02, LAST ANNOTATION UPDATE)

DE HEPOTHETICAL 12.3 ND PROTEIN.

CS HANSENULA POLYNORPRA (TEAST).

CE EURANTOTA: FUGIS I ASCONYCOTINA: HEMIASCONYCETES.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAISPOLIA A.I. SEREZINA S.A. TIRHONIROVA L.P., RETUKE

RANGELIAN A.I. SEREZINA S.A. TIRHONIROVA L.P., RETUKE

BE SEGUENCE 111 AA. 12291 NN; 39D4883A CRC32;

SQ SEQUENCE 111 AA. 12291 NN; 39D4883A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 25

ID 053100 PRELIMINART; PRT; 113 M.

C 053100, ST 05100, ST 051000, ST 05100, ST 051000, 
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|||||||
Qy 699 GASVLGL 705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dec 21 09:28:30 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.6%;
Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.6s, Score 7; DB 3; Length 111;
Best Local Similarity 100.0%; Pred No. 147e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0;
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Best Local Similarity 100 0%; Pred: No. 17e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1998 (TREMDLREL. 01-AUG-1998 (TREMDLREL. 01-AUG-1998 (TREMDLREL. GAG PROTEIN (FRAGMENT).
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|||||||
330 PSTSRPP 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 TSRLRFI 28
|||||||
|640 TSRLRFI 646
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STALEFOLI:
STALEFOLI:
STALEFOLI:
SERVILLEN A.I. SERSINA S.A., TIKHOMIROVA L.P., KRYUKOV V.M.:
SUNMITTED (APR. 1991) TO EMBL/GENBANK/DDBJ DATA BARKS.
DBL: X58862-G2764.
STROMERICAL PROTEEN
SECURENCE 111 AA: 12291 MM; 39D4883A CRC32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOW_TER 125
SEQUENCE 125 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GASSEY N., KIANG E., ARITOSHI K., AMBY P., JENSEN H., DIAS P., WHITTED R. AREVER J. D. EMBL/GENBANK/DDBJ DATA BANKS.
EMBLITTED CART-1999 JO EMBL/GENBANK/DDBJ DATA BANKS.
EMBLITER ACOUSTIS EL197364; ".
ENDLITER 125 125
ENDLITER 125 125
ENDLITER 125 126
     STRAIN-POCESSI;
STRAIN-POCESSI;
KADELNE; 96127539.
KANERO T, TANATA S., SATO S., KOTANI H., SAZUKA T., KIYAJIKA N.,
SGUZURA M., TANATA S., SATO S., KOTANI H., SAZUKA T., KIYAJIKA N.,
DAN RES. 2.1157-166(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EÓUENCE PROM N.A.
TRALHªA;
LANG R., ARIYOSHI K., WILKINS A., DIAS F., WHITTLE H., BREUER J.;
DD RES. HUM. RETROVIRUSES 13:501-505(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAN IMOUNODEFICIENCY VIRUS TYBE 2 (HIV-2).
IHIDAE, 88-RHA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
ENTIVIRINAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125
13505 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07, CREATED)
07, LAST SEQUENCE UPDATE)
07, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 7: DB 14: Length 125:
Pred. No. 1.47e+01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PC04002C CRC32;
                                                                                                                                                                                                                                                                                                          OXYPHOTOBACTERIA; CYANOBACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-951-733-20.rapt
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Mon Dec 21 09:28:30 1998

US-08-951-733-20.rspt

Page 41

Mon Dec 21 09:28:30 1998

US-08-951-733-20.rspt

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Dec 21 09:28:30 1998
US-08-951-733-20.rspt
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Mon Dec 21 09:28:30 1998

US-08-951-733-20.rapt

Page 46

8 Ş 822 Ouery Match 0.6%; Score 7; DB 2; Length 128; Best Local Similarity 100.0%; Pred. No. 1.47e+01; Matches 7; Conservative 0; Mismatches 0; Indels EMBL; D64005; G1006607; -.
HYPOTHETICAL PROTEIN.
SEQUENCE 128 AA; 14443 MW; 2C040B5B CRC32; 0 Caps

RESULT 29

IRESULT 29

IN CORREST PRELIMENT: PRI: 135 AA.

AC 0000239 PRELIMENT: O1 CREATED)

D7 01-80V-1996 (TREMELEEL 01 LAST RESOURCE UPDATE)

D7 01-80V-1996 (TREMELEEL 01 LAST RESOURCE UPDATE)

D7 01-80V-1996 (TREMELEEL 01 LAST RESOURCE UPDATE)

D8 7-CELL LUTENSIAL LIMENSIA TIPE II (CLONE MO-6) TAX-2 (PRAGMENT).

G8 17Ax-2.

G8 17Ax-2.

G8 17Ax-2.

G9 17Ax-2.

G9 17Ax-2.

G9 17Ax-3.

(FRAGMENT).

8

75 SRSLPLP 81 ||||||| 251 SRSLPLP 257

Query Match 0.6%; Best Local Similarity 100.0%; Matches 7; Conservative

Score 7: DB 14: Length 138; Pred. No. 1.47e+01; 0; Mismatches 0: Indels

0;

Gaps

0

SEQUENCE FROM N A.
MEDILINE 9593716:
CINITALE V. D'AGOSTNO D.M., SOTTI L., FRANCHINI G.,
CHIZOLOC PLANCHI L.;
EMBL. 141678, 198239;
EMBL. 141678, 198239;
SEQUENCE 138 AA; 14316 NF; ZAO983AO CRC32;

FELBER

HUMAN T-CELL LYMPHOTROPIC VIRUS TYPE II.
VIRIDAR, SS-RAN, NOMENVELOPED VIRUSES; POSITIVE STRAND RIM, VIRUSES;
RETROVIRIDAE, NOCOVIRINAE, TYPE C ONCOVIRUS GROUP;
MANDALIAN TYPE C ONCOVIRUSES.

RESULT 11

ID 04631;

O4631;

O4631;

O4631;

D7 01. NOV.1996 (TRENDLEEL. 01, CREATED)

D7 01. NOV.1996 (TRENDLEEL. 01, LAST SEQUENCE UPDATE)

D7 01. NOV.1996 (TRENDLEEL. 01, LAST ANNOTATION UPDATE)

D8 KOAL PROTEIN (FRANCEET).

O5 KLEBSIELLA ARGOGRES.

OC EMPERANCELLA ARGOGRES.

OC EMPERANCELLA COLLE.

RE (1)

RE (1

Query Match 0.6%; Score 7; DB 14; Length 135; Best Local Similarity 100,0%; Pred. No. 1.46+01; Indels 0; Matches 7; Conservative 0; Mismatches 0; Indels 0; 72 SRSLPLP 78 ||||||| 251 SRSLPLP 257 Gaps

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TD 98023 PRELIMINARY;
AC 980823 PRELIMINARY;
DT 01-ROY-1996 (TREMBLEEL. 0
DT 01-ROY-1996 (TREMBLEEL. 0
DT 01-ROY-1996 (TREMBLEEL. 0
DT 01-ROY-1996 (TREMBLEEL. 0
DT NOTELN 22/20XIII. PRELIMINARY; 01, CREATED)
01, LAST SEQUENCE UPDATE)
01, LAST ANNOTATION UPDATE) PRT; 138 ζ

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Mon
8
21 09:28:30 1998
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877777777777 094409 PRELIMINARY, PRT; 149 AA.
093400 OT. NOV-1996 (TREMELREL. 01. GREATED)
01. NOV-1996 (TREMELREL. 05. LAST SEQUENCE UPDATE)
01. JUN-1996 (TREMELREL. 05. LAST ANNOTATION UPDATE)
T-CELL LYEMPHOPIC VIRUS TIPE 2 REX AND TAX GENES, PARTIAL CDS, CLONE PUC PX (FRAGRENT).

PRO PX (FRAGMENT).

REY.

REY.

HUMAN T-CELL LYMPHOTRODIC VIRUS TYPE II.

HUMAN T-CELL LYMPHOTRODIC VIRUSES; POSITIVE STRAND |

WIRIDAE; SS-RNA MOMENVELOPED VIRUSES;

RETROVIRIDAE;

MANALIAN TYPE C OMCOVIRUSES. RXA

SECUENCE PROM N.A.
HEDLINE: 9410944.
HEDLINE: 9410944.
OLIVIERA H. D., OLIVIERA O.D., ISHAK R.,
OLIVIERA H. P., LANREIRO P., ISHAK M., ACCYEDO V., HAMMERSHLAK N.,
T. VIROL. 101411494 (1996).
DEPL. 071411494 (1996).
DEPL. 0714711494 (1996).
DEPL. 0714711494 (1996). NON_TER I I SEQUENCE 149 AA; 15702 MW; 483CD5A5 CRC32;

Query Match 0.6%; Best Local Similarity 100.0%; Matches 7; Conservative Score 7; DB 14; Length 149; Pred. No. 1.47e+01; 0; Mismatches 0; Indels 0 Caps 0

밁 86 SRSLPLP 92 |||||||| | 251 SRSLPLP 257

RESULTANCE OF SERVICE OF SERVICE

1ff 13 083393 PRELIMINARY: PRT: 149 AA. 0833939 PREMIREL. 01. CREATED 01-NOV-1996 (TREMELREL. 01. CREATED) 01-NOV-1996 (TREMELREL. 02. LAST SECOUNCE UPDATE) 01-NOV-1996 (TREMELREL. 06. LAST MANOTATION UPDATE) 01-CELL LYEPHOTTODIC VIRUS TYPE 2 REX AND TAX CENSS, PARTIAL CDS, CLONE 0572 (TRAGESEN).

REY.

HUMAN T-CELL LYMPHOTROPIC VIRUS TYPE II.

VIRIDME: SS-RIM MONENVELOPED VIRUSES; POSITIVE STRAND RIA

RETROVIRIIME: ONCOVIRIMAE; TIPE C ONCOVIRUS GROUP;

MANNALIAN TYPE C ONCOVIRUSES.

SEGUENCE FROM N.A.
SEGUENCE FROM N.A.
SEGUENCE PROM N.A.
SEGUENCE PROM

US-08-951-733-20.rapt

Page 47

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Dec 21 09:28:30 1998

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58 LRPSLTG 64 ||||||| 372 LRPSLTG 378

Ouery Match 0.6%; Score 7; DB 2; Length 146; Best Local Similarity 100.0%; Pred. No. 1.47e+01; Matches 7; Conservative 0; Mismatches 0; Indels

6 Gaps

0

146 ; 16712 MW;

RESULT

32

83 B B B EHU S.M., KUBO T., BALL M.M., J. VIEGL. 70.148114921996). EMDL. U2872; G1463038(.) NON_TER 2017. SEQUERCE 149 AA; 15779 NM; 5835635 CRC32;

Query Match 0.6%; Best Local Similarity 100.0%; Matches 7; Conservative Score 7; DB 14; Length 149; Pred. No. 1.47e+01; 0; Mismatches 0; Indels 0

86 SRSLPLP 92 ||||||| 251 SRSLPLP 257

RESULT 34

IN CORRECT PRELIMINARY: PRT: 149 AA.
AC GR3377, PRELIMINARY: PRT: 149 AA.
AC GR3377, PRELIMINARY: PRT: 149 AA.
AC GR3377, PRELIMINARY: PRT: 200224CE UPDATE;
DT 01-1907-1996 (TREMELEEL. 01. LAST RECORDATION UPDATE)
DT 01-1907-1996 (TREMELEEL. 02. LAST AND TAX GENES, PART
DE KT2 (PRACHENT).
GN REX.
OS HUMAN T-CELL LYMPHOTROPIC VIRUS TYPE II.
OC VIRIDAR; SS-RAN HORENTLEDED VIRUSSES; POSITIVE STRAND R
REX.
OC RETROLYRIANE; OCCUTRINAR: TYPE C ONCOVIRUS GROUP;
CR RESULTANE; SS-RAN HORENTLEDED VIRUSSES.
RN [11]
OC RAMALIAN TYPE C ONCOVIRUSES.
RN [12]
RR SEQUENCE FROM N A.
RE STALMANANIANO ZIANCI) PX;
RR SEQUENCE FROM N A.
RE STALMANIANO ZIANCI) PX;
RR MEDILHE: 96190544.
RA ZIANCI N. NOVOA P. MONKEN C., OLIVIERA M.D., OLIVIERA
AN ZIANCI N. NOVOA P. MONKEN C., OLIVIERA M.D., OLIVIERA
AN ZIANCI N. NOVOA P. MONKEN C., OLIVIERA
AN ZIANCI N. NOVOA P. MONKEN C., OLIVIERA
AN ZIANCI N. NOVOA P.
REX. JULIUS N. OLIVIERA M.D., OLIVIERA
AN ZIANCI N. NOVOA P.
REX. JULIUS N. NOVOA P.
RE PARTIAL CDS,

HUMAN T-CELL LYMPHOTROPIC VIRUS TIPE II.
VIRLINA: SS-RNA NORMWELDPED VIRUSES; POSITIVE STRAND RNA VIRUSES
RETROVIRLINAE; ONCOVURINAE; DIPE C ONCOVIRUS GROUP;
NAMMALIAN TIPE C ONCOVIRUSES.

SENDIENCE FROM N.A.
SENDIENCE FROM N.A.
SENDIENCE, 96190544.
EZIRAKU N. NOVAO P., MONKEN C., OLIVIENA N.D., OLIVIERA O.D., ISHAK R.,
DILVIERA M.P., LAUREIRO P., ISHAK M., ACEVEDO V., HAMMERSHIAK N.,
EHU S.R., KUBO T., HALL N. S.
C. VEROL. 70:1481-1482(1996).
EMBL., U22074; 0145044; 7.

EMDI, UD2874; G1403047, MON_TER 1 1 1 3 15748 NW; 3D32851F CRC32; SEQUENCE 149 AA; 15748 NW; 3D32851F CRC32;

Query Match
Best Local Similarity 100.0%;
Matches 7; Conservative Score 7: DB 14: Length 149; Pred. No. 1.47e+01; 0; Mismatches 0; Indels 0; Caps

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₽ 86 SRSLPLP 92 |||||||| 251 SRSLPLP 257

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RESULT 35 ID Q82405

PRELIMINARY;

PRT; 149 ζ

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RESULT 39
REGULT 39
REGULT 39
REGULT 39
REGULT 30
REGULT 39
REGULT 31, CREATED
REGULT 31, LAST SEQUENCE UPDATE)
REGULT 31, LAST SEQUENCE UPDATE
REGULT 31, LAST SEQUENCE TIAGAST.
REGULT 31, REGULT 31, LAST SEQUENCE TIAGAST.
REGULT 32, REGULT 32, REGULT 31, REGULT 32, REGULT 3
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Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100 0%; Pred. Ro. 1.47e+01;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                     Query Match 0.6%;
Best Local Similarity 100.0%;
Matches 7; Conservative
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|||||||
| 251 SRSLPLP 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 36 PRELIMINARY; PRT; 149 AA.
082395; PRELIMINARY; PRT; 149 AA.
082395; OT SON-1996 (TREMBLEEL: 01, CREATED)
01:NOV-1996 (TREMBLEEL: 01, LAST SEQUENCE UPDATE)
10:NOV-1996 (TREMBLEEL: 06, LAST MANOTATION UPDATE)
10:TUT-1996 (TRAMBLEEL: 05, LAST MANOTATION UPDATE)
10:TUT-1996 (TRAMBLEEL: 01, LAST SEQUENCE UPDATE)
10:TUT-1996 (T
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|||||||
401 LPRLPQR 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SENDURKEE FROM N.A.
STRAIN-DANVER HALF-LONG: TISSUE-SOMATIC EMBRYOS AT THE GLOBULAR STRAES.
LIN X., HYANG G.J., EIMCHENGAN J.L.;
SUBHITTED (JAH-1998) TO BEBL/GENBANK/DDBJ DATA BANKS.
BEBL: 047094; G175865; -.
FFAM: PFOOD11, MEPDG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 09:28:30 1998
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NON_TER 1 1 1
SEQUENCE 149 AA; 15672 MM; BA56CDCB CRC32;
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MEDILHE: 96190544.
RETALKU N., NOVAD P., HONKEN C., OLLVIERA M.D., OLIVIERA O.D., ISHAK R.,
CITAKU N., NOVAD P., HONKEN C., ACEVEDO V., HAMMERSHIAK N.,
ZHU S.W., KURD O., HALL W.S.
J. VIROL. 70:1481-1492(1996).
EMBL. URJ2800; 1463108; ...
EMBL. URJ2800; 1463108; ...
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VIRIDAE: SS-RAN MONENVELOPED VIRUSES; POSITIVE STRAND RNA VIRUSES;
RETROVIRIDAE; DOCOVIRINE, TYPE C ONCOVIRUS GROUP;
HAMMALIAN TYPE C ONCOVIRUSES.
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01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 05, LAST SHWOTATION UPDATE)
01-UPL-1998 (TREMBLREL. 05, LAST SHWOTATION UPDATE)
T-CELL LYMPHOTATION TIPE 2 REX AND TAX GENES, PARTIAL CDS, CLONE
PAR PX (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; E73147; E245470; .
SEQUENCE 167 AA; 19759 MW; SABBF574 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-ROY-1996 (TREMBLEEL. 01, CREATED)
01-ROY-1996 (TREMBLEEL. 01, LAST SEQUENCE UPDATE)
01-NOY-1996 (TREMBLEEL. 07, LAST ANNOTATION UPDATE)
01-NOG-1996 (TREMBLEEL. 07, LAST ANNOTATION UPDATE)
18A7-SHOCK COCKATE (FRAGMENT).
DAUGUS CAROTA (CARROY).
DAUGUS CAROTA (CARROY).
EMBRYONTA: PLANTA: EMBRYOPHTIA; ANGIOSPERMAE; DICOTYLEDONEAE; APIALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIMAN T-CELL LYAPHOTROPIC VIRUS TYPE II.
VIRIDAE: 55-RNA NONENVELOPED VIRUSES: POSITIVE STRAND RNA VIRUSES:
RETROVIRIDAE: DENCOVIRINAE: TYPE C ONCOVIRUS GROUP;
MANALIAN TYPE C ONCOVIRUSES.
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STRAIN-SPI PJ.
S
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JEDLER H., WEDLER E., SCHARFE M., WAMBUTT R.;
JEDHITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                       36 DGLLLRL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BELLIFERAE.
                                                                                                                                                                                 Score 7; DB 3; Length 167;
Pred. No. 1.47e+01;
0; Mismatches 0; Indels
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Pred. No. 1.47e+01;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-951-733-20.rapt
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RESULT 41

IRESULTS 41

PRELIMINARY; PRT; 170 AA.
AC 073444,
DT 01-340-1998 (TREMCLEEL 07, CREATED)
DT 01-340-1998 (TREMCLEEL 07, LAST SEQUENCE UPDATE)
DT 01-340-1998 (TREMCLEEL 07, LAST ANDOTATION UPDATE)
DE REX PROTEIN.
GN REX.

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ID 20

ID 20
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ID Q39680
AC Q39680;
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Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cuery Match 0.6%; Score 7: DB 14; Length 149;
Best Local Similarity 100 0%; Pred. No. 1.47e+01;
Matches 7; Conservative 0; Mismatches 0; Indels
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No. 1.47e+01; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. VIROL. 70:1481-1492(1996).
EMEL: U22873; G1465Q41; -.
NON TER
1 1 7 7BIADWAG CRC32;
SEQUENCE 149 AA; 15764 MM; 7BIADWAG CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. TISCET-MERY CORD: TISCET-MERY CORD: TISCET-MERY CORD: SET OF THE SET 
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1082399 PRELIMINARY: PRT: 149 M.
1082399: 101-WOV-1996 (TREMBLEEL: 01. CREATED)
101-WOV-1996 (TREMBLEEL: 02. LAST SEQUENCE UPDATE)
101-WOV-1996 (TREMBLEEL: 05. LAST SEQUENCE UPDATE)
101-WOW-1996 (TREMBLEEL: 05. LAST SEQUENCE)
101-WOW-1996 (TREMBLEEL: 05. LAST SEQUENCE)
102-WOW-1996 (TREMBLEEL: 05. LAST SEQUENCE)
103-WOW-1996 (TREMBLEEL: 05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 GLPAPGA 20
|||||||
237 GLPAPGA 243
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251 SRSLPLP 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 149 AA; 15779 MW;
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SERALMANANIA (TANT.) PX:
SERALMANANIA (TANT.) PX:
SERALMAN N. MOYON, D. MONKEN C., OLIVIENA M.D., OLIVIENA O.D., ISHAN R.,
DETARMAN M. MOYON, D., MONKEN C., OLIVIENA M.D., OLIVIENA M.P., LAUREIRO P., ISHAN M., ACEVEDO V., RAMBESSHLAN N.,
SEN S. W., MODO ST., SHALL W.W.,
SEN S. W., MODO ST., SHALL W.W.,
SEN S., SHALL W.W.,
SEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HUMAN T-CELL LYMPHOTROPIC VIRUS TYPE II.
VIRIDAE; SS-RUA NONEWVELOPED VIRUSES; PÓSITIVE STRAND RUA
RETROVIRIDAE; ONCOVIENUE; TYPE C ONCOVIEUS GROUP;
MANDALIAN TYPE C ONCOVIEUSES.
                       SEQUENCE FROM N.A.
LEPOGRAPHER F.;
SUBMITIED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYMAN T-CELL LYMPHOTROPIC VIRUS TYPE 2B.
VIRUSES: RETROLID VIRUSES; RETROVIRIDAE; BLV-HTLV RETROVIRUSES;
HUMAN T-CELL LYMPHOTROPIC VIRUS TYPE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       882 DGLLLRL 888
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ETOURNEUR F., D'AURIOL L., DAZEA M.C., PETEZRS M., BEDJABAGA I.,
IOT P., DELAGORTE E., GESSAIN A., MONPLAISIR N.;
CEN. VIROL. 79:269-277(1999).
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Pred. No. 1.47e+01;
0; Mismatches 0; Indels
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RESULTS 42

RESULTS 42

RESULTS 42

DESCRIPTION OF THE MALLER. 10. CREATED)

DT 01.MVV-1996 (TREMBLEEL. 01. LAST SEQUENCE UPDATE)

DE REX 26 ED PROTEIN.

OS HUMAN T-CELL LYHHOTMOPIC VIRUS TUPE 11.

OS HUMAN T-CELL LYHHOTMOPIC VIRUS TUPE 11.

OS HUMAN T-CELL LYHHOTMOPIC VIRUS PUBLIC SEGUENCE

OC MANALIAN TYPE C ONCOVIRUS GROUP;

OC MANALIAN TYPE C ONCOVIRUS SES.

RE SEQUENCE PROM N.

RE SEQUENCE PROM N.

RE SEQUENCE PROM N.

RE SEQUENCE PROM N.

RE SEQUENCE SEGUEN SEGUENCE N. SHINISU N. GOJOBORI T., GOLDE D.

RA SHINOTONIO N. TAKAHASHI Y. SHINISU N. GOJOBORI T., GOLDE D.

RA SHINOTONIO S. TAKAHASHI Y. SHINISU N. GOJOBORI T., GOLDE D.

RA SHINOTONIO S. TAKAHASHI Y. SHINISU N. GOJOBORI T., GOLDE D.

RA SHINOTONIO S. TAKAHASHI Y. SHINISU N. GOJOBORI T., GOLDE D.

RA SHINOTONIO S. TAKAHASHI Y. SHINISU N. GOJOBORI T., GOLDE D.

RA SHINOTONIO S. TAKAHASHI Y. SHINISU N. GOJOBORI T., GOLDE D.

RA SHINOTONIO S. TAKAHASHI Y. SHINISU N. GOJOBORI T., GOLDE D.

RA SHINOTONIO S. TAKAHASHI Y. SHINISU N. GOJOBORI T., GOLDE D.

RA SHINOTONIO S. TAKAHASHI Y. SHINISU N. GOJOBORI T., GOLDE D.

RA SHINOTONIO S. TAKAHASHI Y. SHINISU N. GOJOBORI T., GOLDE D.

RA SHINOTONIO S. TAKAHASHI Y. SHINISU N. GOJOBORI T., GOLDE D.

RA SHINOTONIO S. TAKAHASHI Y. SHINISU N. GOJOBORI T., GOLDE D.

RA SHINIS R. L., TECCH N., YARMOR H., COPPIN J.;

RA SEQUENCE PROM N. A.

ROSERVA YARMOR MADONANONI, COLD SPRIMG HARBOR (1895).

RA ROSERVA PROM N. A.

ROSERVA T. J., A.

ROSERVA T. J., A.

RA ROSERVA T. J., A.
                                                                                                                                Dec 21 09:28:30 1998
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Best Local Similarity 100.0%; Pred. No. 1.47e+01;
Matches 7; Conservative 0; Mismatches 0; Indels
    Query Match 0.6%;
Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.6%;
Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 0.6%; Score 7; DB 14; Length 170;
Best Local Similarity 100 0%; Pred. No. 1.47e+01;
Matches 7; Conservative 0; Mismatches 0; Indels
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505935 PRELIMINARY;
Q56935;
Q1-80V-1996 (TREMBLREL 01, CO) 1-80V-1996 (TREMBLREL 01, CO) 1-80V-1996 (TREMBLREL 01, CO)
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251 SRSLPLP 257
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|||||||
856 GSILSTL 862
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STEMITTED (NOY-1986) TO EMBL/GENBANK/DDBJ DATA BANKS
EMBL, M10060: G319560; ...
SEQUENCE 170 AA; 18463 MW; 00011EB2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEPOLENCE FROM R.A.
STRAINFAILH;
MU PA, BLLICOTT J., MCCREADY P., SKOHRONSKI E., GARNES J.,
KOBAYASHI A., CARRANO A.V., BRÜBAKZE R., GARCIA E.;
KOBAYASHI A., CARRANO A.V., BRÜBAKZE R., GARCIA E.;
KOBAYASHI PAS 1998) TO BELÇGERBANK/DDSJ DAYA BAKKS.
ERBL; APOS 3946; G 2996 260; ...
FERBL; APOS 3946; G 2996 260; ...
PASKHI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PERSINIA PESTIS.
PLASKID PODI.
PROKANTOYA: GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
ENTEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEDOURICE PROM N.A.
HEDLINE: 85116449.
SETMODONNO: T., PARABASHI Y., SHINIZU N., GOJOBORI T., GOLDE D.R.,
CHEN 15., MTA. N., SUGLMURA T.,
PROC. NATL. ACAD. SSI. U.S.A. 62:3101-3105(1985).
                                                                                                                                                                                                                                                                                                                                 EQUIENCE FROM N.A.
EDILINE: 95286274.
CLESTRON A., NOSQVIST R., WOLF-WATZ H., FORSBERG
INFECT. IMMUN. 63:2269-2276(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SECURENCE PROM N.A.

REDLINE: 64550196 R., PERKINS D., BRIGGS D., LEE T.H., ESSEX H.

SOURBONSKI J., PATARCH F., CALLOR R.C., RASENTINE W.A.;

SCIENCE 23:41-43(198).
                                                                                                                                                                                       BÖUENCE FROM N.A.
IOLASTRYM A.M.;
IOBATTEED (DEC-1994) TO EMBL/GENBANK/DDBJ DATA BANKS
IOBATTEED (DEC-1994); -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RSINIA PSEUDOTUBERCULOSIS.
ASMID PIB1.
ROKARYOTA; GRACILICUTES; SC
TYEROBACTERIACEAE.
                                                                                                                                182 AA; 20999 MW; C744A6FD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CREATED)
LAST SEQUENCES ANNOUNCES
    Score 7; DB 2; Length 182;
Pred. No. 1.47e+01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 7; DB 2; Length 182;
Pred. No. 1.47e+01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-951-733-20.rapt
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         o.
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RESULT 46

053143 PRELIMINAT; PH

045145 PR

015404 PR

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ID 971395;
AC 971395;
AC 971395;
AC 971395;
DT 01-FEB-1997 (TREMBLARE, 02, L
DT 01-FEB-1997 (TREMBLARE, 02, L
DT 01-AGG-1998 (TREMBLARE, 02, L
DT 01-AGG-1998 (TREMBLARE, 02, L
DE HIFFORMATICAL,
GN HITEGORY
COS HARMOFFRILIS HELICOTTES;
AC PROCHATOTAL, GRACILICOTTES;
AC PROCHATOTAL, GRACILICOTTES;
AC PROCHATOTAL, GRACILICOTTES;
AC PROCHATOTAL GRACILICOTTES;
AC REMANDAGE A.R. SUTTON G., FUTUR
BA METEMBER A. SUTTON G., FUTUR
BA METEMBER A. SUTTON G., FUTUR
BA ACCOUNT JO., SHIRLER R., L. LOU L
BA ACCOUNT JO., SHIRLER R., L. LOU L
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ID 068704

AC 068704;

DT 01-AUG-1998 (
DT 01-AUG-1998 (
DT 01-AUG-1998 (
DT 01-AUG-1998 (
DE YOPK (YOPQ)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ş
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Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.6%;
Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97 GSLRTAQ 103
|||||||
1116 GSLRTAQ 1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SECURNCE FROM N.A.

NAKAYMAK K.I., TOKITO S., NAKAUCHI H., GACHELIN G.;

LIMDINGGENETICS 0:0-0(0).

EMCLI. D90146: E38881: -.

FRAM: PFO0129: HMC_I.

SEQUENCE 184 AA; 21191 MM; 8545770D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107 SRSLPLP 113
|||||||
251 SRSLPLP 257
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HEDLINE, 930444.
HEDLINE, 930444.
HEDLINE, 1016ER K.B., SHANSON P., ADARICIO J.J., CHIN K.K., LAX J.P.,
NGUTEN M., MANT J. LECKIE G., ZANETTI A., MARINGCEI G., CHEN I.S.Y.,
NGUTEN M., MANT J. L.,
VIROLOCY 196:57-69(1993).
EMBL; L11456; G3464041.
EMBL; L120734, G404041.
EMBL; L120734, G404041.
EMBL; L20734, G404041.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 09:28:30
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VINIDAE: SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
OKCOVIRIMAE:
    ESOCIENCE FROM N.A.

REDLINE, 93306 NA.

REDLINE, 93306 NA.

RELINORANN R.D., AAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,

RELLAVAGE A.R., BULT C.J., TOMB J.F., DOUGLERTY B.A., MERACK J.M.,

KERLAVAGE A.R., BULT C.J., TOMB J.F., DOUGLERT C.A., GOCANE J.D.,

KKERMER K., SUTTON G., FITZHOGH W., FIZLAS C.A., GOCANE J.D.,

SCOTT J.D., SHILLER R., LUI U.I., GLODER A., KELLEY J.M., WEIDMAN J.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SECURNCE FROM N.A.
KEDLINE; 9332307.
NARDI D., SWITZER W.M., HADLOCK K.G., KAPLAN J.E., LAL R.B.,
POLES T.M.
27 VIROL. 67:4659-4664(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 SRSLPLP 113
|||||||
251 SRSLPLP 257
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|||||||
| 856 GSILSTL 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 (TREMBLREL. 07,
8 (TREMBLREL. 07,
8 (TREMBLREL. 07,
) HOMOLOG (YOPQ).
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                                                                                                                                                                                                                                                            SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 7; DB 14; Length 170;
Pred. No. 1.47e+01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                       CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 7; DB 11; Len
Pred. No. 1.47e+01;
0; Mismatches 0;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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Page 53

Mon Dec 21 09:28:30 1998

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GASAWARA N.; UBMITTED (APR-1997) TO EMBL/GENBANK/DDBJ

DAIE Y., YATA K., FUJITA M., SÁGAI H... ASAWARA W.: BHITTED (APR-1997) TO EMBL/GEMBANK/DDDJ

SAGAI H., ITAYA M., KASAHARA Y.,

DATA BANKS.

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RESULT 49

RESULT 49

DO C. 198560 (TRESULEZI. 0). CREATED)

DO C. 1990 (TRESULEZI. 0). CREATED)

DO C. 1990 (TRESULEZI. 0). ANT SEQUENCE UPDATE)

DO C. 1990 (TRESULEZI. 0). TAST SEQUENCE

DO C. 1990 (TRESULEZI. 0). TAST SEQUENCE

C. 1990 (TRESULEZI. 0). TAST SEQUENCE

DO C. 1990 (TRESULEZI. 0). TAST SEQUENCE

R. 11

R. 1
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RESULT 50
ID 017563
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                                                                                                                                                                                                                                                                                                                                                                                            PROTENCE PROM N.A.

PROTENCE PROM N.A.

WILSON R., ANISCOUGH R., ANDERSON K., BANNES C., BERKS M., BONFIELD J.,

A BURNOW J., CONNELL M., COPSET T., COOPER J., COULSON A., CRANTON M.,

A BURNOW J., CONNELL M., COPSET T., COOPER J., COULSON A., CRANTON M.,

A BURNOW J., CONNELL M., COPSET T., COOPER J., CARDER A., CREEN P.,

A MARKINS T., BURNING M., JUEN M., JOHNSON J., LOWES M., KERSIAN J.,

KATERIA J., LAISTEN N., JATRELLE P., LICHTWINE J., LUCTO C.,

A KATORNAK N., MORTINGE B., O'CALGRANN M., PRESONS J., EPROT C.,

A KATORNAK N., SANDERS D., SIGNAMERS R., SMALDON M., SMITH A.,

A KATORNAK N., SANDERS D., SIGNAMERS R., SMALDON M., SMITH A.,

A KATORNAK N., SANDERS D., SIGNAMERS R., SMALDON M., SMITH A.,

A KATORNAK N., SANDERS D., SIGNAMERS R., SMALDON M., WEINSTOCK L.,

A WILKINGON SPROAT J., WHILDMAN P.,

MEDIC JANGES ENGAGE.

M. MOLTRA D. SANDERS D., SIGNAM P.,

MEDIC JANGES ENGAGE.

M. MOLTRA D. SANDERS D., SIGNAM P.,

M. MOLTRA D. SANDERS D.,

SANDERS D. SANDERS D.,

M. MOLTRA D. SANDERS D. SANDERS D.,

M. MOLTRA D
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 0.6%; Score 7; DB 2; Length 192; Best Local Similarity 100,0%; Pred. No. 1.476+07; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                 Query Match 0.6%; Score 7; DB 5; Length 206; Best Local Smilarity 100 0%; Pred No 1.47e+01; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105 VIGAYDT 111
1111111
735 VIGAYDT 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 TFLRTLY 76
|||||||
904 TFLRTLY 910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17. 48

OOSSO3 PRELIMINANY; PRT; 205 AA.

OOSSO3, PREMIMENT; PRT; 205 AA.

OL-JUL-1997 (TREMSLEEL, O4, CREATED)

OL-JUL-1997 (TREMSLEEL, O4, LAST SEQUENCE UPDATE)

OL-JUN-1998 (TREMSLEEL, O6, LAST ANNOTATION UPDATE)

MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SECUENCE FROM N.A., KERLAVAGE A.R., FLEISCHMANN R.D.;
WHITE O., CLAYON R.A., KERLAVAGE A.R., FLEISCHMANN R.D.;
SCHMITTEED (SEP-1996) OP EMEL/GENHANK/DDBJ DATA BANKS.
EMEL. U13841; 51574535; SECUENCE 192 AA; 20590 NH; 43A5EB6A CRC12;
                                                                                                                                           135 LFDVFLR 141
||||||
827 LFDVFLR 833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŠEĆUZNCE PROM N.A.
STRAIN=168;
SADAIE Y., YATA K., FUJITA M., SAGAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRILLIPS CA., SPRIGGS T. HEDBLOM E., COTTON M.D., UTTERBACK T.R.,
BANNA M.C., MOUTER D.T., SAUDER D.M., BANNDOM R.C., PIPE L.D.,
PRITCHEMAN J.L., PRASEN C.M., SMITH H.O., VENTER J.C.;
SCIENCE 209-466-512(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ECUENCE PROM N.A.
TATUSOV R., HUSHEGIAN A.R., BORK P., BROWN N.P., HAYES W.S.,
DRODOVSKY M., RUDD K.E., KOONIN E.V.;
11R., BIOL. 6:279-231(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCILLUS SUBTILIS.
NCIANTOTA: PIRMICUTES; ENDOSPORE-PORMING RODS AND COCCI; BACILLACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOUBNEE FROM N.A.

EISCEMANN R.D., ADAMS N.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,

EISCEMANN R.D., ADAMS N.D., WHITE O., CLAYTON R.A., KERAICK J.M.,

RILANGE A.R., BULT C.J., TOMB J.F., DOUGHERT B.A., MERRICK J.M.,

CKENNEY K., SUTTON G., FITZHIGH W., FIELDS C.A., GOCKNEE J.D.,

CKENNEY K., SUTTON G., FITZHIGH W., FIELDS C.A., GOCKNEE J.D.,

ILLITS C.A., SPRIGGS T., HEDBLOM E., COTYON H.D., UTTERBACK T.R.,

NINA M.C., KOUTEN D.T., SADDEK D.M., BRANDON R.C., FIRE L.D.,

NINA M.C., KOUTEN D.T., SADDEK D.M., BRANDON R.C., FIRE L.D.,

COMALD L.A., SHALL K.V., FRASER C.M., SHITH B.O., VENTER J.C.;

BHITTED (JUL-1995) TO EMBL/CENBANK, DEBJ DATA BANKS.
PRELIMINARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 1.47e+01;
0; Mismatches 0; Indels
PRT;
209 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H., ITAYA M., KASAHARA Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-951-733-20.rspt
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                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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RE RESTLER RE RESTLER R
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Query Match 0 0.6; Score 7; DB 5; Length 209;
Best Local Similarity 100.0%; Pred. No. 147e+01; 148e-04;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                              SEDUMENCE FROM N.A.
WILSON R. ANDERSON K. BAYRES C. BERKS M. BONFIELD J.
BURTON J. COMPELL M. CORPET L. COLORD J. COLORDA M. CERATON M.
DEAR S. DU S. DURBIN R. FAVELLO A. FULTON L. CARDINE M. GREEN P.
BARKINS T. ALTER W. LATER M. JOHNSTON M. JONES M. KERSINN J.
KIESTEN J. ASTER N. LATERILLE P. DISSTON M. JONES M. KERSINN J.
KIESTEN J. MOSTEROS B. C. CALLAGRAN M. PARSONS J. LLOTD C.
BITKEN L. RODPAN M. SANDRES D. STONMELTE M. SALLON N. SMITH M.
COMBANDER E. STADER R. SULSTON J. THIEREY-MIEG J. THOMS K.
VALCHAN K. VALCHAN K. HATHERYON B. MATSON A. WEINSTOCK L.
VALCHAN M. PARSONS J. NOLLDMAN P.;
NATURE 368 123 281 1987121.
NATURE 368 123 281 1987121.
NATURE 368 123 281 1987121.
NOLLER SELSEN E. 187721.
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01-JAN-1998 (TREMBLREL 05, CI
01-JAN-1998 (TREMBLREL 05, LI
01-JAN-1998 (TREMBLREL 05, L
01-JAN-1998 (TREMBLREL 05, L
F07B10.3 (TREMBLREL)
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STRAIN-16:

STRAIN-16:
                                                                                                                                                                                                                                                                                   SEQUENCE 209 AA; 24388 MW; 80CFFAA2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 09:28:30
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Raryota: Metazoa: acoelomates: Nematoda; secernentea:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.6%; Score 7; DB 2; Length 205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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